

Shears, Beverly

From: Devi, Sarvamangala
Sent: Wednesday, April 23, 2003 7:37 AM
To: Shears, Beverly
Subject: 09/711,896

Good morning Beverly:

Would you please perform a sequence and an interference search for SEQ ID NO: 1 in application SN 09/711,896?

Thanks.

S. DEVI, Ph.D.
AU 1-645
CM1-7E15

TE/2
MB

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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100-500000-100

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: _____
Searcher: _____
Terminal time: 25
Elapsed time: _____
CPU time: _____
Total time: 28
Number of Searches: _____
Number of Databases: 2

Search Site

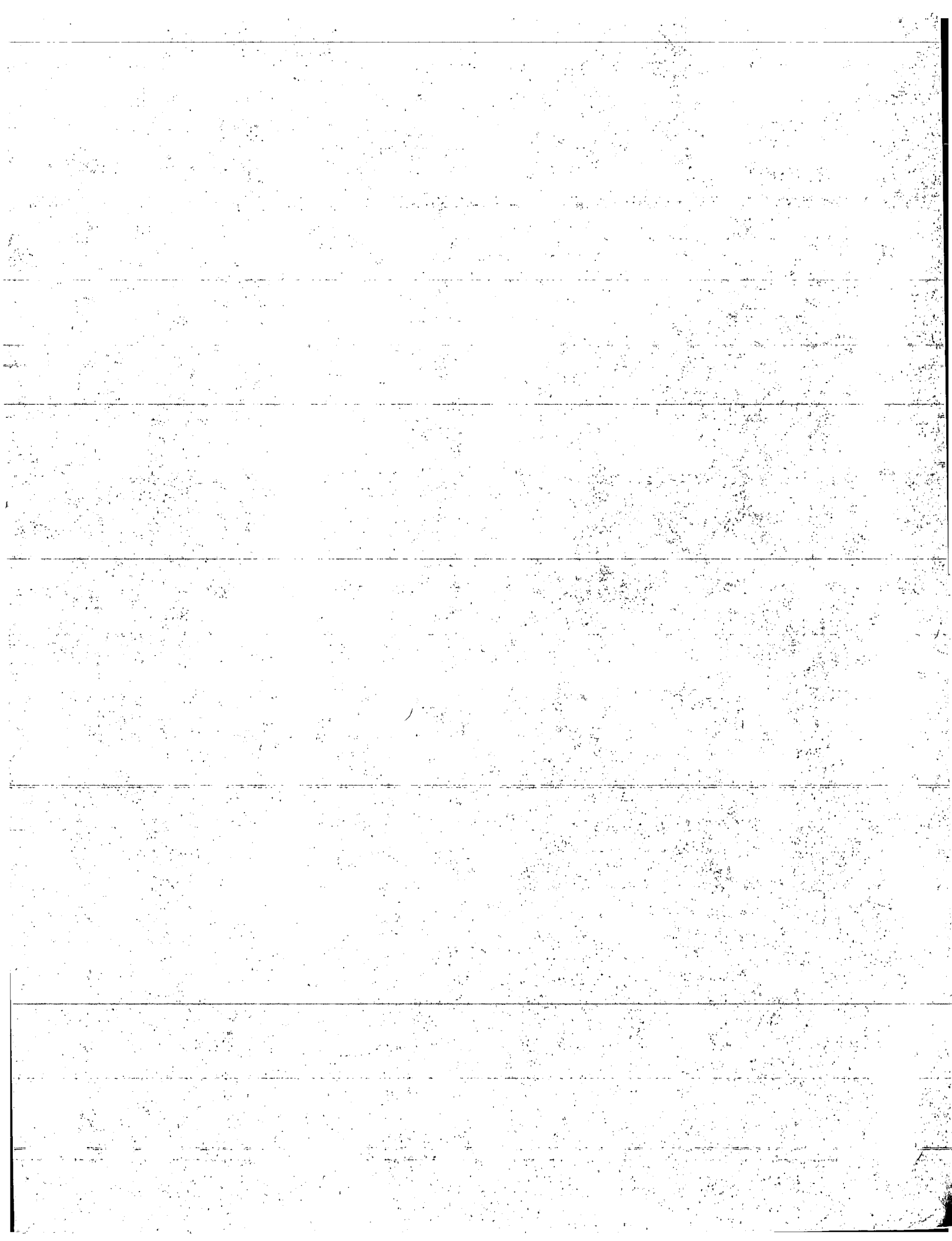
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ ☒ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ ☒ Other CGN



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 35 Seconds
(without alignments)
137.058 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAEPVEDNCINEVAMKFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5.

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
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3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	36	22 AAB82406	Human interleukin-
2	188	100.0	41	19 AAB37739	An N-terminal frag
3	188	100.0	41	19 AAW52171	Interferon-gamma i
4	188	100.0	193	17 AAR99560	Human interferon-g
5	188	100.0	193	18 AAW31757	Interferon gamma i
6	188	100.0	193	18 AAW22047	Interferon gamma i
7	188	100.0	193	19 AAW77082	Interleukin 18 act
8	188	100.0	193	19 AAW37740	Interferon-gamma i
9	188	100.0	193	19 AAW52172	Interferon-gamma i
10	188	100.0	193	19 AAW47429	Interferon-gamma p

11	188	100.0	193	19 AAW46592	Amino acid sequenc
12	188	100.0	193	21 AAY53908	Amino acid sequenc
13	188	100.0	193	22 AAB82409	Human interleukin-
14	188	100.0	193	22 AAG63830	Amino acid sequenc
15	188	100.0	193	23 AAE16953	Human precursor in
16	188	100.0	536	23 AAE16957	Human pro-IL-18/ca
17	188	100.0	588	23 AAE16958	Human pro-IL-18/ca
18	185	98.4	193	22 AAB30541	A human IL-18 with
19	179	95.2	193	22 AAY72608	Macaca cynomolgus
20	162	86.2	42	18 AAW22049	Interferon gamma i
21	159	84.6	193	21 AAY58241	Equine interleukin
22	147.5	78.5	192	22 AAG78713	Pig protein. Sus
23	147.5	78.5	192	22 AAG64653	Porcine interleukin
24	136	72.3	193	21 AAY58240	Canine interleukin
25	132	70.2	193	20 AAY01314	Canine interleukin
26	132	70.2	193	21 AAY82558	Canine interleukin
27	132	70.2	193	21 AAY82560	Canine interleukin
28	110	58.5	35	22 AAB82407	Mouse interleukin-
29	110	58.5	192	22 AAB82411	Mouse interleukin-
30	110	58.5	192	23 ABB57087	Mouse ischaemic co
31	109	58.0	175	19 AAW53283	Amino acid sequenc
32	109	58.0	194	19 AAW53282	Amino acid sequenc
33	62.5	33.2	1398	21 AAB18292	Plasmodium falcipa
34	55	29.3	274	23 ABP01892	Human ORFX protein
35	52	27.7	151	22 AAU16278	Human novel secret
36	52	27.7	156	22 ABB27680	Human peptide #331
37	52	27.7	156	22 ABB32850	Peptide #356 encod
38	52	27.7	156	22 ABB18332	Protein #331 encod
39	52	27.7	156	22 AAM66036	Human bone marrow
40	52	27.7	156	22 AAM13905	Peptide #339 encod
41	52	27.7	156	22 AAM26311	Peptide #348 encod
42	52	27.7	156	22 AAM01648	Peptide #330 encod
43	52	27.7	156	23 ABG35684	Human peptide enco
44	52	27.7	445	22 ABB30835	Peptide #3486 enco
45	52	27.7	445	22 ABB30993	Peptide #3644 enco

ALIGNMENTS

RESULT 1

ID AAB82406 standard; Peptide; 36 AA.

XX AAB82406;

XX AC AAB82406;

XX DT 06-AUG-2001 (first entry)

XX DE Human interleukin-18 precursor propeptide sequence.

XX KW Interleukin-18; antibody; human; infection; tumour; sarcoma;

XX KW autoimmune disease; therapy; diagnosis; detoxification.

XX OS Homo sapiens.

XX PN EP1101772-A1.

XX PD 23-MAY-2001.

XX PF 15-NOV-2000; 2000EP-0310121.

XX PR 16-NOV-1999; 99JP-0324860.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;

XX DR WPI; 2001-368892/39.

XX PT New antibodies specific to interleukin 18 (IL-18) precursor, useful in manufacturing a medicament for treating IL-18-related diseases, e.g. autoimmune disease, or for detecting, eliminating or detoxifying the precursor

XX Claim 5; Page 13; 27pp; English.
 PS The present sequence is that of the propeptide region of the
 CC human interleukin-18 (IL-18) precursor. Monoclonal and polyclonal
 CC antibodies specific to the human IL-18 precursor propeptide are
 CC claimed. These are useful in detection and purification of IL-18
 CC precursor, and in the elimination and detoxification of the
 CC precursor accumulated in vivo. Detection methods using the
 CC antibody are effective in qualitative and quantitative analyses for
 CC the precursor, and also in the correction of imprecise results
 CC obtained from assays using anti-IL-18 antibody, which exhibit
 CC cross-reactivity against the precursor. Pharmaceutical compositions
 CC comprising an antibody specific to the IL-18 precursor can be used
 CC to treat viral infections including AIDS, bacterial infections,
 CC solid malignant tumours, malignant tumours of haemocytes, sarcomas,
 CC autoimmune disease, hepatopathy, pancreatopathy, and diseases of
 CC the gallbladder, kidney and nervous system. Detection methods
 CC using the antibody can be used to diagnose such diseases.

Sequence 36 AA;

Query Match 100.0%; Score 188; DB 22; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.1e-21;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

RESULT 2

AAW37739
 ID AAW37739 standard; Protein; 41 AA.

XX AC AAW37739;

XX DT 07-JUL-1998 (first entry)

XX DE An N-terminal fragment of interferon-gamma inducing precursor peptide.

XX KW Interferon-gamma inducing precursor peptide; IFN-gamma;
 KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
 KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.

XX OS Mammalia.

XX EP821005-A2.

PD 28-JAN-1998.

XX 18-JUL-1997; 97EP-0305376.

XX 31-JAN-1997; 97JP-0031474.

PR 25-JUL-1996; 96JP-0213267.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Tanimoto T;

DR WPI; 1998-088847/09.

DR NPSDB; AAV18906.

XX Conversion of interferon-inducing polypeptide precursor to active
 PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
 PT useful for, e.g. enhancing cytotoxicity by killer cells

XX Claim 1; Page 14; 18pp; English.

XX This is the amino acid sequence for an N-terminal fragment of the
 CC interferon-gamma (IFN-gamma) inducing precursor peptide, which is
 CC cleaved to form the active mature protein when it is in contact with
 CC interleukin-1-beta-converting enzyme (ICE). The polypeptide is used

CC for inducing, e.g. production of IFN-gamma a useful biologically
 CC active substance, enhancing cytotoxicity by, and inducing the
 CC formation of killer cells. The polypeptide may potentially be used
 CC as an antiviral, antitumour and immunopathy agent and as an antiseptic.

XX Sequence 41 AA;

Query Match 100.0%; Score 188; DB 19; Length 41;
 Best Local Similarity 100.0%; Pred. No. 4.8e-21;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36
 |||||

Db 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

RESULT 3

AAW52171
 ID AAW52171 standard; peptide; 41 AA.

XX AC AAW52171;

XX DT 10-JUN-1998 (first entry)

XX DE Interferon-gamma inducing polypeptide precursor N-terminal fragment.

XX KW Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.

XX OS Homo sapiens

XX FH Key Location/Qualifiers

FT Cleavage-site 36..37

FT /note- "an enzyme cleaves the linkage between Asp
 FT and Tyr to convert the precursor into its
 FT active form"

XX EP819757-A2.

XX 21-JAN-1998

XX 18-JUL-1997; 97EP-0305377.

XX 30-MAY-1997; 97JP-0156062.

PR 19-JUL-1996; 96JP-0207691.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Tanimoto T;

XX WPI; 1998-078838/08.

XX Polypeptide-processing enzyme - for preparing mature form of
 PT interferon-inducing polypeptide

XX Claim 2; Page 14; 18pp; English.

XX This is the N-terminal fragment of a precursor of an interferon-gamma
 CC (IFN-gamma) inducing polypeptide. The polypeptide induces IFN-gamma
 CC production in immunocompetent cells [the polypeptide is not named but
 CC is described in JP 27198/96 and 193098/96]. An enzyme can convert the
 CC precursor form into its active form by cleaving a linkage between Asp
 CC at amino acid position 36 and Tyr at amino acid position 37 of this
 CC fragment. The enzyme can be obtained from a human haematopoietic cell
 CC and can be inhibited by iodoacetamide, and acetyl-L-tyrosyl-L-valyl-L-
 CC alanyl-L-aspart-L-al. The enzyme can be used for cleaving a recombinant
 CC IFN-gamma pro-polypeptide to form a mature polypeptide.

XX Sequence 41 AA;

Query Match 100.0%; Score 188; DB 19; Length 41;
 Best Local Similarity 100.0%; Pred. No. 4.8e-21;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36
 |||
 Db 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36

RESULT 4

AAAR99560
 ID AAR99560 standard; Protein; 193 AA.

XX AC AAR99560;

XX DT 29-SEP-1996 (first entry)

XX DE Human interferon-gamma inducer protein.

XX KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..36

XX FT Protein /label= Leader_peptide

XX FT Misc-difference 109

XX FT /label= Mat_protein

XX FT /label= Ile, Thr

XX PN EP712931-A2.

XX XX 22-MAY-1996.

XX PD 10-NOV-1995; 95EP-0308055.

XX PF 29-SEP-1995; 95JP-0274988.

XX PR 15-NOV-1994; 94JP-0304203.

XX PR 23-FEB-1995; 95JP-0058240.

XX PR 10-MAR-1995; 95JP-0078357.

XX PR 18-SEP-1995; 95JP-0262062.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;

XX PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;

XX DR WPI; 1996-252837/26.

XX DR N-PSDB; AAT32404.

XX PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful

XX PT to treat and prevent, e.g. viral disease, malignancies and immune

XX PT disorders

XX PS Claim 6; Page 41-42; 48pp; English.

XX CC The mature portion of a novel human protein, (AAR99560) induces

XX CC interferon-gamma (IFN-gamma) prodn. by immunocompetent cells. It

XX CC is the product of a cDNA clone (AAT32404) obtd. from a human liver

XX CC library. The protein enhances the cytotoxicity of killer cells

XX CC and/or induces the formation of killer cells (e.g. NK cells,

XX CC lymphokine-activating killer (LAK) cells, and cytotoxic T-cells).

XX CC The mature protein (see also AAR99558) is useful as an antiviral,

XX CC antitumor, antibacterial, immunoregulatory and blood platelet

XX CC enhancing agent, and can be used in adoptive immunotherapy. It is

XX CC also used to raise monoclonal antibodies.

XX SQ Sequence 193 AA;

XX Query Match 100.0%; Score 188; DB 17; Length 193;

XX Best Local Similarity 100.0%; Pred. No. 3e-20;

XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36
 |||
 Db 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36

RESULT 5

AAW31757
 ID AAW31757 standard; Protein; 193 AA.

XX AC AAW31757;

XX DT 15-JAN-1998 (first entry)

XX DE Interferon gamma inducing factor-2 (IGIF-2) R140I variant.

XX KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte; human;
 KW inflammation; proliferation; differentiation; maturation; tissue damage.

XX OS Homo sapiens;

XX FH Key Location/Qualifiers

XX FT Misc-difference 140

XX FT /label= R140I

XX FT /note= "Wild type Arg is replaced by Ile"

XX PN WO9724441-A1.

XX PD 10-JUL-1997.

XX PF 20-DEC-1996; 96WO-US20432.

XX PR 29-DEC-1995; 95US-0580667.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Cocks BG, Coleman R, Hawkins PR;

XX DR WPI; 1997-363677/33.

XX DR N-PSDB; AAT74988.

XX PT Novel interferon gamma inducing factor-2 - used to screen for

XX PT compounds to diagnose, treat or prevent tissue damage associated

XX PT with inflammation

XX PS Claim 3; Page -; 60pp; English.

XX CC This protein sequence represents an interferon gamma inducing factor-2

XX CC (IGIF-2) variant, identified from a liver cDNA library. This sequence

XX CC differs from IGIF-2 identified from a T-lymphocyte cDNA library

XX CC (AAW220477), in that amino acid 140 is found to be changed from Arg to

XX CC Ile. A second variant, AAW22049, also exists. Probes derived from the

XX CC nucleic acid sequences can be used to quantify the expression of IGIF-2

XX CC in conditions that are associated with inflammation or aberrant

XX CC expression of IGIF-2. The protein can be used to screen for compounds

XX CC that interact with IGIF-2, such as antibodies, antagonists or other

XX CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2

XX CC expression or activity. The protein can also be used to diagnose, prevent

XX CC or treat IGIF-2 induction of proliferation, differentiation or maturation

XX CC of leucocytes or lymphocytes, especially in relation to tissue damage

XX CC associated with inflammation.

XX CC Note:- This sequence does not appear in the specification; it has

XX CC been made by modifying the IGIF-2 sequence presented in AAW22047.

XX SQ Sequence 193 AA;

XX Query Match 100.0%; Score 188; DB 18; Length 193;

XX Best Local Similarity 100.0%; Pred. No. 3e-20;

XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFAEDDENLESD 36

KW	Chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism
XX	Homo sapiens.
OS	Key Location/Qualifiers
XX	Peptide 1..36 "Signal peptide"
FT	Peptide 37..193
FT	/note= "Mature peptide"
XX	EP861663-A2.
PN	02-SEP-1998.
XX	24-FEB-1998; 98EP-0301352.
PD	25-FEB-1997; 97JP-0055468.
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA	Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX	WPI: 1998-448964/39.
XX	N-PSDB; V4828.
DR	Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX	of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT	osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
PT	primary hyperthyroidism and osteoporosis
XX	Disclosure: Page 24-28; 56pp; English.
PS	Interleukin-18 (IL-18) or a functional equivalent can be used for
XX	inhibition of osteoclast formation. IL-18 is used for treating or
CC	preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC	Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC	arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC	osteoporosis.
XX	-Sequence 193 AA;
SO	Query Match 100.0%; Score 188; DB 19; Length 193;
	Best Local Similarity 100.0%; Pred. No. 3e-20;
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1 MAAPVEDNCINFAVKFIDNTLYFIADDDENLESD 36
Db	
	1 MAAPVEDNCINFAVKFIDNTLYFIADDDENLESD 36
RESULT 8	
AAW37740	
ID	AAW37740 standard; Protein; 193 AA.
XX	AC AAW37740;
XX	07-JUL-1998 (first entry)
DE	Interferon-gamma inducing precursor peptide.
XX	Interferon-gamma inducing precursor peptide; IFN-gamma;
KW	Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
KW	antiviral agent; antitumour agent; immunopathy agent; antiseptic.
XX	Mammalia.
OS	Key Location/Qualifiers
XX	Protein 36..157
FT	/note= "Mature protein"
FT	Misc-difference 109
FT	/label= Ile, Thr
FT	Cleavage-site 36..37

PN EP821005-A2.
 XX 28-JAN-1998.
 PD 18-JUL-1997; 97EP-0305376.
 PF 31-JAN-1997; 97JP-0031474.
 PR 25-JUL-1996; 96JP-0213267.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kurimoto M, Tanimoto T;
 XX WPI; 1998-088847/09.
 DR N-PSDB; AAV18906.
 XX Conversion of interferon-inducing polypeptide precursor to active
 PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
 PT useful for, e.g. enhancing cytotoxicity by killer cells
 XX Claim 2; Pages 14-15; 18pp; English.
 PS This is the amino acid sequence for the interferon-gamma (IFN-gamma)
 CC inducing precursor peptide, which is cleaved to form the active mature
 CC protein when it is in contact with interleukin-1-beta-converting
 CC enzyme (ICE). The polypeptide is used for inducing, e.g. production
 CC of IFN-gamma. A useful biologically active substance, enhancing
 CC cytotoxicity by, and inducing the formation of killer cells. The
 CC polypeptide may potentially be used as an antiviral, antitumour and
 CC immunopathy agent and as an antiseptic.
 XX Sequence 193 AA;
 SQ Query Match 100.0%; Score 188; DB 19; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 RESULT 9
 AAW52172
 ID AAW52172 standard; peptide; 193 AA.
 AC AAW52172;
 XX 10-JUN-1998 (first entry)
 DT Interferon-gamma inducing polypeptide precursor sequence.
 DE Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Peptide 1..36
 FT Peptide /label= sig_peptide
 FT Peptide 37..193
 FT Misc-difference 109 /label= mat_peptide
 XX EP816499-A2.
 PN 07-JAN-1998.
 PD 27-JUN-1997; 97EP-0304616.
 PF 27-JUN-1996; 96JP-0185305.
 PR (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA Kurimoto M, Okura T, Torigoe K;
 PI WPI; 1998-054914/06.
 DR N-PSDB; AAV15825; AAV15826.
 XX Genomic DNA encoding polypeptide inducing interferon-gamma
 PT production - by immuno-competent cells, useful to treat e.g. human
 PT malignant tumours or viral diseases
 XX

DR WPI; 1998-078838/08.
 DR N-PSDB; AAV17200.
 XX polypeptide-processing enzyme - for preparing mature form of
 PT interferon-inducing polypeptide
 XX Claim 3; Page 15; 18pp; English.
 PS This sequence represents the precursor of an interferon-gamma (IFN-gamma)
 CC inducing polypeptide. The polypeptide induces IFN-gamma production in
 CC immunocompetent cells [the polypeptide is not named but is described in
 CC JP 27198/96 and 193098/96]. An enzyme can convert this precursor form
 CC into its active form by cleaving a linkage between Asp at amino acid
 CC position 36 and Tyr at amino acid position 37 of its N-terminal fragment.
 CC The enzyme can be obtained from a human haematopoietic cell and can be
 CC inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-aspart
 CC -1-al. The enzyme can be used for cleaving a recombinant IFN-gamma
 CC pro-polypeptide to form a mature polypeptide.
 XX Sequence 193 AA;
 SQ Query Match 100.0%; Score 188; DB 19; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 RESULT 10
 AAW47429
 ID AAW47429 standard; Protein; 193 AA.
 AC AAW47429;
 XX 05-JUN-1998 (first entry)
 DT Interferon-gamma production inducer.
 DE Interferon-gamma; IFN-gamma; production inducer; gene therapy;
 XX immunocompetent cell; treatment; prevention; malignant tumour;
 KW viral infection; bacterial infection; immune disease.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..36
 FT Peptide /label= sig_peptide
 FT Peptide 37..193
 FT Misc-difference 109 /label= mat_peptide
 XX EP816499-A2.
 PN 07-JAN-1998.
 PD 27-JUN-1997; 97EP-0304616.
 PF 27-JUN-1996; 96JP-0185305.
 PR (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA Kurimoto M, Okura T, Torigoe K;
 PI WPI; 1998-054914/06.
 DR N-PSDB; AAV15825; AAV15826.
 XX Genomic DNA encoding polypeptide inducing interferon-gamma
 PT production - by immuno-competent cells, useful to treat e.g. human
 PT malignant tumours or viral diseases
 XX

PS Claim 2; Pages 49-50; 74pp; English.

CC The present sequence is a protein, which induces

CC interferon-gamma (IFN-gamma) production in immunocompetent cells.

CC The protein has high biological activity, including enhancing

CC cytotoxicity of killer cells and inducing killer cell formation,

CC in addition to inducing IFN-gamma production by immunocompetent

CC cells when expressed in mammalian cells, facilitating its use in

CC low dosages to treat/prevent, e.g. malignant tumours, viral or

CC bacterial infections and immune diseases. As it is expressed in

CC mammalian cells, it also has low toxicity when used in human

CC treatments, minimising side effects. The DNA encoding the protein

CC can be used in gene therapy, e.g. by infecting vectors containing

CC the DNA or transplanting cells.

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 188; DB 19; Length 193;

Best Local Similarity 100.0%; Pred. No. 3e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 11

AAW46592

XX ID AAW46592 standard; Protein: 193 AA.

XX AC AAW46592;

XX 21-MAY-1998 (first entry)

XX Amino acid sequence of human interleukin-1-gamma.

KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;

KW induction; antibody; diagnostic assay; fusion protein; activity;

KW immunological disorder; allergy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 41..47 "beta-1 region"

FT /note= "beta-1 region"

FT Region 55..59

FT /note= "beta-2 region"

FT Region 64..68

FT /note= "beta-3 region"

FT Region 83..88

FT /note= "beta-4 region"

FT Region 96..102

FT /note= "beta-5 region"

FT Region 108..113

FT /note= "beta-6 region"

FT Region 115..120

FT /note= "beta-7 region"

FT Region 137..143

FT /note= "beta-8 region"

FT Region 147..153

FT /note= "beta-9 region"

FT Region 160..164

FT /note= "beta-10 region"

FT Region 170..175

FT /note= "beta-11 region"

FT Region 187..191

FT /note= "beta-12 region"

XX W09744468-A1.

XX 27-NOV-1997.

XX 16-MAY-1997; 97WO-US07282.

XX 20-MAY-1996; 96US-0651998.

XX (SCHE) SCHERING CORP.

XX Bazan JF; Hardiman GT; Kastelein RA; Sana TR; Timans JC;

XX WPI; 1998-018522/02.

XX N-PSDB; AAV05368.

XX Antagonist of human interleukin-1-gamma - used for treating

XX immunological disorders caused by human IL-1-gamma.

XX PS Disclosure; Pages 54-55; 63pp; English.

XX The present sequence represents human interleukin-1-gamma (IL-1-gamma).

CC The protein is the human equivalent of a mouse cytokine, IGIF, which

CC induces certain T cells to produce interferon-gamma. Human IL-1-gamma

CC and mouse IGIF show 71% identity at the nucleotide level and

CC approximately 65% identity at the amino acid level. Antagonists of

CC IL-1 gamma, e.g. antibodies, can be used in a method for treating a

CC condition caused by human IL-1 gamma. The antibodies can also be used

CC in diagnostic assays. The IL-1 gamma protein can be covalently

CC conjugated to polyethylene glycol or to a polypeptide, and the fusion

CC protein used in a pharmaceutical composition for supplying the

CC biological activity of IL-1 gamma. Conditions that can be treated using

CC the human IL-1-gamma protein include immunological disorders, allergies,

CC and infectious diseases. The IL-1-gamma can also be used to detect the

CC presence of the protein or its receptor.

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 188; DB 19; Length 193;

Best Local Similarity 100.0%; Pred. No. 3e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 12

AAV53908

XX ID AAV53908 standard; Protein: 193 AA.

XX AC AAV53908;

XX 13-MAR-2000 (first entry)

XX Amino acid sequence of a protein that induces IFN-gamma production.

XX Human; interferon gamma production; IFN-gamma; immunocompetent cell;

XX antiviral; immunoregulatory; antigen; mitogen;

XX IFN-gamma susceptible disease; antibacterial; antitumour;

XX blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;

XX AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;

XX renal cancer; mycosis; fungoides; chronic granulomatous disease;

XX blood cell malignant tumour; adult T cell leukaemia;

XX chronic myelogenous leukaemia; malignant leukaemia; immune disease

XX allergy; rheumatism.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..36

FT /note= "signal peptide"

FT Protein 37..193

FT /note= "mature protein"

FT Misc-difference 109

FT /label= Ile, Thr

FT /note= "encoded by AYT"

XX EP962531-A2.

XX PD 08-DEC-1999.
 XX PF 10-NOV-1995; 99EP-0104104.
 XX PR 15-NOV-1994; 94JP-0304203.
 XX PR 23-FEB-1995; 95JP-0058240.
 XX PR 10-MAR-1995; 95JP-0078357.
 XX PR 18-SEP-1995; 95JP-0262062.
 XX PR 29-SEP-1995; 95JP-0274988.
 XX PR 10-NOV-1995; 95EP-0308055.
 XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX PI Ushio S, Torigoe K, Tanimoto T, Okamura H;
 XX N-PSDB; AAZ36876.
 XX WPI; 2000-064289/06.
 XX DR N-PSDB; AAZ36876.
 XX PT Novel polypeptides used in the treatment of interferon-gamma
 XX susceptible diseases
 XX PS Example A-4-3; Page 7; 42pp; English.
 XX CC The present sequence represents a human protein that induces interferon
 CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
 CC protein which has antiviral, antitumor and immunoregulatory activities,
 CC and is produced by immunocompetent cells stimulated with antigens or
 CC mitogens. The protein of the invention is used to treat IFN-gamma
 CC susceptible diseases, and also have use as a antiviral agent,
 CC antibacterial agent, antitumor agent, immunoregulatory agent and blood
 CC platelet enhancing agent. Diseases which can be treated with the
 CC protein include viral diseases such as hepatitis, herpes syndrome,
 CC condyloma, and AIDS; bacterial diseases such as Candidiasis and
 CC malaria; solid malignant tumours such as renal cancer, mycosis
 CC fungoides, and chronic granulomatous disease; blood cell malignant
 CC tumours such as adult T cell leukaemia, chronic myelogenous leukaemia,
 CC and malignant leukaemia; and immune diseases such as allergy and
 CC rheumatism.
 XX SQ Sequence 193 AA:
 Query Match 100.0%; Score 188; DB 21; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 ||||||||||||||||||||||||||||||||||||
 DB 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 RESULT 13
 AAB82409
 ID AAB82409 standard; Protein; 193 AA.
 XX AC AAB82409;
 XX DT 06-AUG-2001 (first entry)
 XX DE Human interleukin-18 precursor.
 XX KW Interleukin-18; antibody; human; infection; tumour; sarcoma;
 KW autoimmune disease; therapy; diagnosis; detoxification.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX PE Peptide I..36
 XX FT Protein /label= Signal_peptide
 XX FT /label= Mature_protein
 XX FT Misc-difference 109
 XX FT /label= Ile, Thr

XX EP1101772-A1.
 XX PD 23-MAY-2001.
 XX PF 15-NOV-2000; 2000EP-0310121.
 XX PR 16-NOV-1999; 99JP-0324860.
 XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX PI Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;
 XX WPI; 2001-368892/39.
 XX DR N-PSDB; AAF90444.
 XX PT New antibodies specific to interleukin 18 (IL-18) precursor, useful in
 XX manufacturing a medicament for treating IL-18-related diseases, e.g.
 XX autoimmune disease, or for detecting, eliminating or detoxifying the
 XX precursor
 XX PS Example 1-2; Page 14-15; 27pp; English.
 XX CC The present sequence is that of human interleukin-18 (IL-18)
 CC precursor. Monoclonal and polyclonal antibodies specific
 CC to the human IL-18 precursor propeptide (see AAB82406) are
 CC claimed. These are useful in detection and purification of IL-18
 CC precursor, and in the elimination and detoxification of the
 CC precursor accumulated in vivo. Detection methods using the
 CC antibody are effective in qualitative and quantitative analyses for
 CC the precursor, and also in the correction of imprecise results
 CC obtained from assays using anti-IL-18 antibody, which exhibit
 CC cross-reactivity against the precursor. Pharmaceutical compositions
 CC comprising an antibody specific to the IL-18 precursor can be used
 CC to treat viral infections including AIDS, bacterial infections,
 CC solid malignant tumours, malignant tumours of haemocytes, sarcomas,
 CC autoimmune disease, hepatopathy, pancreatopathy, and diseases of
 CC the gallbladder, kidney and nervous system. Detection methods
 CC using the antibody can be used to diagnose such diseases.
 XX SQ Sequence 193 AA:
 Query Match 100.0%; Score 188; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 ||||||||||||||||||||||||||||||||||||
 DB 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLESD 36
 RESULT 14
 AAG63830
 ID AAG63830 standard; Protein; 193 AA.
 XX AC AAG63830;
 XX DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of human interleukin 18 (IL-18).
 XX KW T-cell-helper type 2 response; Th2 response; T cell mediated response;
 KW allergic response; interleukin 18; IL-18; IGE-mediated allergy;
 KW allergic asthma; anaphylactic reaction; asthma associated allergy;
 KW IGE dependent allergic rhinoconjunctivitis.
 XX OS Homo sapiens.
 XX PN WO200168896-A1.
 XX PD 20-SEP-2001.
 XX PF 02-MAR-2001; 2001WO-US06869.

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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 : Search time 29 seconds
(without alignments)
36.525 Million cell updates/sec

Title: us-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMRFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	41	2	US-08-896-605A-1
2	188	100.0	41	2	US-08-896-501A-1
3	188	100.0	193	2	US-08-896-605A-2
4	188	100.0	193	2	US-08-896-501A-2
5	188	100.0	193	4	US-08-832-180-9
6	179	95.2	193	4	US-09-597-576-2
7	50	26.6	536	4	US-08-653-648A-13
8	49	26.1	747	3	US-08-089-397A-16
9	49	26.1	776	1	US-07-603-133B-17
10	49	26.1	776	1	US-07-603-133B-20
11	49	26.1	776	3	US-08-089-397A-15
12	48.5	25.8	464	1	US-07-991-867B-2
13	48.5	25.8	464	1	US-08-107-755A-2
14	48.5	25.8	464	2	US-08-544-332-2
15	48.5	25.8	464	4	US-09-370-861A-2
16	48	25.5	688	4	US-09-113-750A-3
17	47	25.0	475	4	US-09-213-247C-4
18	47	25.0	694	2	US-08-895-522-4
19	47	25.0	694	3	US-09-193-391-4
20	47	25.0	775	1	US-07-603-133B-15
21	47	25.0	775	1	US-07-603-133B-16
22	46	24.5	266	4	US-09-414-276-8
23	46	24.5	1170	2	US-08-789-078-2
24	46	24.5	1170	2	US-08-752-633-2
25	46	24.5	1170	2	US-08-476-082A-42
26	46	24.5	1170	5	PCT-US95-04886-2
27	46	24.5	1170	5	PCT-US96-01314-42

28	46	24.5	2409	6	5180808-2
29	45	23.9	322	4	US-09-080-205-8
30	45	23.9	365	2	US-08-204-288-7
31	45	23.9	395	4	US-09-134-001C-5119
32	45	23.9	906	1	US-08-486-270-2
33	45	23.9	906	3	US-08-367-264-2
34	45	23.9	906	4	US-09-153-757-2
35	45	23.9	906	5	PCT-US91-09422-17
36	45	23.9	1056	2	US-08-687-289A-7
37	45	23.9	1056	2	US-08-687-289A-8
38	45	23.9	1058	2	US-08-687-289A-5
39	45	23.9	1194	4	US-08-538-526-1
40	45	23.9	1199	1	US-08-041-538-2
41	45	23.9	1199	1	US-08-463-642-2
42	45	23.9	1199	1	US-08-455-602-2
43	45	23.9	1199	2	US-08-465-157-2
44	45	23.9	1199	5	PCT-US91-09422-2
45	44.5	23.7	137	4	US-09-134-001C-4731

ALIGNMENTS

RESULT 1

US-08-896-605A-1

; Sequence 1, Application US/08896605A

; Patent No. 5879942

; GENERAL INFORMATION:

; APPLICANT: TANIMOTO, Tadao

; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/896,605A

; FILING DATE: 18 July 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 207,691/1996

; FILING DATE: 19-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 156,062/1997

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: TANIMOTO=2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 41 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal fragment

; US-08-896-605A-1

Query Match

Best Local Similarity 100.0%; Score 188; DB 2; Length 41;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10

[illegible]

FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 100.0%; Score 188; DB:2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36
|||||
Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 5

US-08-832-180-9
Sequence 9, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpei
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 100.0%; Score 188; DB:4; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36
|||||
Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 6

US-09-597-576-2
Sequence 2, Application US/09597576
Patent No. 6432678
GENERAL INFORMATION:
APPLICANT: Alexander Taylor
APPLICANT: Han Trinh
TITLE OF INVENTION: MACACA CYNOMOLGUS IL18
FILE REFERENCE: GP-70629
CURRENT APPLICATION NUMBER: US/09/597,576
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/140,140
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2:
LENGTH: 193
TYPE: PRT
ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

Query Match 95.2%; Score 179; DB:4; Length 193;
Best Local Similarity 94.4%; Pred. No. 2.3e-19;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36
|||||
Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 7

US-08-653-648A-13
Sequence 13, Application US/08653648A
Patent No. 6379945
GENERAL INFORMATION:
APPLICANT: Jepson, Ian
APPLICANT: Greenland, Andrew
APPLICANT: Martinez, Alberto
TITLE OF INVENTION: A Gene Switch
FILE REFERENCE: PPD50047/US
CURRENT APPLICATION NUMBER: US/08/653,648A
CURRENT FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: GB 9510759.5
PRIOR FILING DATE: 1995-05-26
PRIOR APPLICATION NUMBER: GB 9605656.9
PRIOR FILING DATE: 1996-03-18
PRIOR APPLICATION NUMBER: GB 9513882.2
PRIOR FILING DATE: 1995-07-07
PRIOR APPLICATION NUMBER: GB 9517316.7
PRIOR FILING DATE: 1995-08-24
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 536
TYPE: PRT
ORGANISM: Chironomus tentans
US-08-653-648A-13

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-603-133B-20

Query Match 26.1%; Score 49; DB 1; Length 776;
Best Local Similarity 52.6%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KFIDNTLYFAEDDENLES 35
||| | | :||| ||:
Db 666 KFIPNRAYRVKDEVLEA 684

RESULT 11
US-08-089-397A-15
Sequence 15, Application US/08089397A
Patent No. 6086880
GENERAL INFORMATION:
APPLICANT: SABARA, MARTA I. J.
APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: IGJAZ, MOHAMMAD K.
APPLICANT: GILCHRIST, JAMES E.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUL-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 29311-20003.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-089-397A-15

Query Match 26.1%; Score 49; DB 3; Length 776;
Best Local Similarity 52.6%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KFIDNTLYFAEDDENLES 35

Db 666 KFIPNRAYRVKDEVLEA 684
||| | | :||| ||:

RESULT 12
US-07-991-867B-2
Sequence 2, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-991-867B-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INEVAMKF---IDNTLYFI 26
||| | | :||| ||:

Db 20 INFMSMLFFSKIDNMVYFI 38
||| | | :||| ||:

RESULT 13
US-08-107-755A-2
Sequence 2, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI14.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-755A-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26
||||| | | | | | |
Db 20 INFMSMLFFSKIDNMYFI 38

RESULT 14
Sequence 2, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UFI14.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-544-332-2

Query Match 25.8%; Score 48.5; DB 2; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26
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Db 20 INFMSMLFFSKIDNMYFI 38

RESULT 15
US-09-370-861A-2
Sequence 2, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UFI14.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Amsacta moorei entomopoxvirus
US-09-370-861A-2

Query Match 25.8%; Score 48.5; DB 4; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26

Db 20 INFMMLFFSKIDNNVPI 38

Search completed: April 23, 2003, 08:19:06
Job time : 31 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:19:14 ; Search time 42 Seconds
(without alignments)
68.683 Million cell updates/sec

Title: US-09-711-896A-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMKFIDNTLYFAIEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	193	9	US-09-770-528-8
2	188	100.0	193	10	US-09-798-075-1
3	176	93.6	193	9	US-10-094-153-3
4	176	93.6	193	9	US-10-094-153-4
5	176	93.6	193	9	US-10-094-153-5
6	176	93.6	193	9	US-10-094-153-9
7	139.5	74.2	133	10	US-09-917-265-2
8	139.5	74.2	192	10	US-09-917-265-8
9	110	58.5	192	9	US-09-770-528-9
10	52	27.7	151	10	US-09-764-864-1231
11	52	27.7	156	10	US-09-864-761-33630
12	52	27.7	445	10	US-09-864-761-46601
13	52	27.7	445	10	US-09-864-761-47605
14	50	26.6	78	9	US-09-749-637A-318
15	49	26.1	285	10	US-09-815-242-4869
16	49	26.1	334	10	US-09-815-242-10798
17	48.5	25.8	264	9	US-09-738-626-5729
18	48.5	25.8	3712	9	US-10-108-605-103
19	47.5	25.3	1806	10	US-09-919-497-56

Sequence 4, Appli
Sequence 39, Appli
Sequence 37, Appli
Sequence 146, Appli
Sequence 2, Appli
Sequence 1447, Ap
Sequence 3369, A
Sequence 32, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 442, App
Sequence 92, Appli
Sequence 6, Appli
Sequence 12, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 430, App
Sequence 124, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App

US-09-770-528-8
Sequence 8, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines: Related Reagents
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:

ALIGNMENTS

RESULT 1

US-09-770-528-8

Sequence 8, Application US/09770528

Patent No. US20020164332A1

GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.

Sana, Theodore R.

Kastelein, Robert A.

TITLE OF INVENTION: Mammalian Cytokines: Related Reagents

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,528

FILING DATE: 25-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/130,972

FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/055,111

FILING DATE: 06-AUG-1997

APPLICATION NUMBER: US 09/062,866

FILING DATE: 20-APR-1998

APPLICATION NUMBER: US 09/097,976

FILING DATE: 16-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0725K2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match 100.0%; Score 188; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36

RESULT 2

US-09-798-075-1
Sequence 1, Application US/09798075
Patent No. US2001004418A1
GENERAL INFORMATION:
APPLICANT: Levy, Shoshana
APPLICANT: Dekryuff, Rosemarie
APPLICANT: Umetsu, Dale
APPLICANT: Maeker, Hoiden
TITLE OF INVENTION: Treatment of Allergies
FILE REFERENCE: STAN-179
CURRENT APPLICATION NUMBER: US/09/798,075
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/188,311
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-075-1

Query Match 100.0%; Score 188; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36

RESULT 3

US-10-094-153-3
Sequence 3, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-798-075-1

OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-3

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENIE 34

RESULT 4

US-10-094-153-4
Sequence 4, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-4

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
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1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENIE 34

RESULT 5

US-10-094-153-5
Sequence 5, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-5

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENIE 34

Db 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 34

RESULT 6

US-10-094-153-9

; Sequence 9, Application US/10094153

; Patent No. US20020169291A1

; GENERAL INFORMATION:

; APPLICANT: Dinarello, Charles

; APPLICANT: Kim, Soo Hyun

; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use

; FILE REFERENCE: 475

; CURRENT APPLICATION NUMBER: US/10/094,153

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: 60/274,327

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Artificial Sequence.

; FEATURE:

; OTHER INFORMATION: Synthetic PRT Sequence

US-10-094-153-9

Query Match 93.6%; Score 176; DB 9; Length 193;

Best Local Similarity 97.1%; Pred. No. 3.1e-17;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENLE 34

|||||

Db 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 34

RESULT 7

US-09-917-265-2

; Sequence 2, Application US/09917265

; Patent No. US20020052030A1

; GENERAL INFORMATION:

; APPLICANT: Wonderling, Raman S.

; APPLICANT: Boroughs, Karen L.

; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE

; FILE REFERENCE: IM-5

; CURRENT APPLICATION NUMBER: US/09/917,265

; CURRENT FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: 60/223,016

; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Felis catus

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (119)..(119)

; OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.

; NAME/KEY: misc.feature

; LOCATION: (470)..(470)

; OTHER INFORMATION: n = unknown at position 470

; OTHER INFORMATION: Xaa = unknown at position 119

US-09-917-265-2

Query Match 74.2%; Score 139.5; DB 10; Length 133;

Best Local Similarity 75.0%; Pred. No. 2.6e-12;

Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENLES 36

|||||

Db 1 MTAIPVDD-CINFVGMKFDINTLYFVADSDENLETD 35

RESULT 8

US-09-917-265-8

; Sequence 8, Application US/09917265

; Patent No. US20020052030A1

; GENERAL INFORMATION:

; APPLICANT: Wonderling, Raman S.

; APPLICANT: Boroughs, Karen L.

; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

; FILE REFERENCE: IM-5

; CURRENT APPLICATION NUMBER: US/09/917,265

; CURRENT FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: 60/223,016

; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Felis catus

US-09-917-265-8

Query Match 74.2%; Score 139.5; DB 10; Length 192;

Best Local Similarity 75.0%; Pred. No. 4e-12;

Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENLES 36

|||||

Db 1 MTAIPVDD-CINFVGMKFDINTLYFVADSDENLETD 35

RESULT 9

US-09-770-528-9

; Sequence 9, Application US/09770528

; Patent No. US20020164332A1

; GENERAL INFORMATION:

; APPLICANT: Hedrick, Joseph A.

; Sana, Theodore R.

; Bazan, Fernando J.

; Kastelein, Robert A.

; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents

; and Methods

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/770,528

; FILING DATE: 25-Jan-2001

; CLASSIFICATION: <Unknown>

; PRT APPLICATION DATA:

; APPLICATION NUMBER: 09/130,972

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/055,111

; FILING DATE: 06-AUG-1997

; APPLICATION NUMBER: US 09/062,866

; FILING DATE: 20-APR-1998

; APPLICATION NUMBER: US 09/097,976

; FILING DATE: 16-JUN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0725K2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-770-528-9

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Query Match      58.5%; Score 110; DB 9; Length 192;
Best Local Similarity. 66.7%; Pred. No. 5.3e-08;
Matches 20; Conservative 5; Mismatches 5; Indels
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7	EDNCINFVAMKFIDNTLYFIAEDDENL	36
6	EDSCVNFKEMMFIDNTLYFIEPENGDL	35

RESULT 10 ..
US-09-764-864-1231
; Sequence 1231, Application
; Patent No. US20020132753A1
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 1231
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; US-09-764-864-1231

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1 MAAPEVEDNCINFVAMKFIDNT 22.
:::|::| |::|::|
122 LSVHNIEESCFOFLKFKFLDST 143
db

RESULT 11
 US-9864-761-33630
 Sequence 33630, Application
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED
 FILE REFERENCE: Aemica-x-1
 CURRENT APPLICATION NUMBER: US/09/864.7
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6

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PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33630
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000241.1
OTHER INFORMATION: EXPRESSED IN HELIX, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.9
OTHER INFORMATION: EST_HUMAN HIT: A1652927.1, EVALUO 9.00e-25
OTHER INFORMATION: SWISSPROT HIT: A14867, EVALUO 2.00e-89
OTHER INFORMATION: EST_HUMAN HIT: A0134963.1, EVALUO 1.00e-69

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QY	1	MAAEPVEDNCINFVAMKFIDNT	22
Db	12	LSVHNIEESCFOFLKFKFLDST	33

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RESULT 12
US/09-864-761-46601
: Sequence 46601, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED
: TITLE OF INVENTION: GENE EXPRESSION A
: FILE REFERENCE: Aomic-a-x-1
: CURRENT APPLICATION NUMBER: US/09/864,

```


APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US 09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46601
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF00201.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALUATE 1.00e-130
OTHER INFORMATION: SWISSPROT HIT: Q14867, EVALUATE 0.00e+00
US-09-864-761-46601

Query Match 27.7%; Score 52; DB 10; Length 445;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY : 1 MAEPVEDNCINFVAMKFDINT 22
DB 35 LSVHNIEESCQFLKPKFLDST 56

RESULT 13

US-09-864-761-47605
Sequence 47605, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US 09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47605
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF124731.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
OTHER INFORMATION: SWISSPROT HIT: Q14867, EVALUATE 0.00e+00
OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALUATE 1.00e-130
US-09-864-761-47605

Query Match 27.7%; Score 52; DB 10; Length 445;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY : 1 MAEPVEDNCINFVAMKFDINT 22
DB 35 LSVHNIEESCQFLKPKFLDST 56

RESULT 14
US-09-749-637A-318

; Sequence 318, Application US/09749637A
; Patent No. US2002017349A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Watkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 318
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Conus imperialis
; US-09-749-637A-318

Query Match 26.6%; Score 50; DB 9; Length 78;
Best Local Similarity 34.8%; Pred. No. 4.7;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 10 CINFVAMKFIDNTLYFIAEDDEN 32
I: ||| I: : : : I: I:
Db 5 CVFVAVPFLTASVFITADSRN 27

RESULT 15
US-09-815-242-4869
; Sequence 4869, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4869
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-815-242-4869
Query Match 26.1%; Score 49; DB 10; Length 285;
Best Local Similarity 33.3%; Pred. No. 28;
Matches 10; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
Qy 6 VEDNCINFVAMKFIDNTLYFIAEDDEN 35
I: ||| I: : : : I: I:
Db 69 IQDMLVELENTNFIDTILFLDADDEELVS 98
Search completed: April 23, 2003, 08:25:16
Job time : 43 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 43 seconds
(without alignments)
80.485 Million cell updates/sec

Title: US-09-711-896A-1
Perfect score: 186
Sequence: 1 MAADPVEDNCINFVAMKFDNTLYFIAEDDENLESD 36
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	58.5	192	2 S60226	cytokine IGIF - mo
2	62.5	33.2	1398	2 H71606	hypothetical prote
3	56	29.8	780	2 T29700	hypothetical prote
4	55	29.3	275	2 G89961	hypothetical prote
5	55	29.3	687	2 S3485	carnitine O-acetyl
6	53	28.2	365	2 E81307	succinyl-diaminopi
7	52.5	27.9	212	2 G97866	hypothetical prote
8	52	27.7	736	2 T00023	transcription fact
9	51	27.1	647	2 T28214	probable nucleosid
10	50	26.6	302	2 T38789	hypothetical prote
11	50	26.6	536	2 A36590	ecdysteroid recept
12	50	26.6	908	2 A22254	hypothetical prote
13	49.5	26.3	1009	2 T16604	hypothetical prote
14	49	26.1	327	2 E97088	beta-xylosidase, f
15	49	26.1	338	2 A82890	hypothetical prote
16	49	26.1	490	2 H96911	uroporphyrinogen I
17	49	26.1	747	1 VPAR4S	outer layer protei
18	49	26.1	776	1 VPAR4S	outer layer protei
19	49	26.1	776	1 VPARB3	outer layer protei
20	49	26.1	776	2 S24410	hypothetical outer
21	49	26.1	1628	2 T38055	hypothetical prote
22	48.5	25.8	285	2 T09308	immediate-early pr
23	48.5	25.8	299	2 J64374	sterol uptake prot
24	48.5	25.8	384	2 F81354	DNA /pantothenate
25	48.5	25.8	464	1 WZVZG1	GIL protein - Amsa
26	48.5	25.8	1218	2 T31376	glutamate receptor
27	48.5	25.8	3712	2 S18253	laminin alpha-1 ch
28	48	25.5	209	2 H90128	hypothetical prote
29	48	25.5	480	2 T34102	hypothetical prote

30	47.5	25.3	284	2 A83688	hypothetical prote
31	47.5	25.3	367	2 T19937	hypothetical prote
32	47.5	25.3	482	2 B31795	collagen alpha 1(X
33	47.5	25.3	532	2 T02539	hypothetical prote
34	47.5	25.3	673	2 T15551	hypothetical prote
35	47.5	25.3	888	2 S28791	collagen alpha 1(X
36	47.5	25.3	1435	2 S34697	DNA polymerase III
37	47.5	25.3	1435	2 C90596	hypothetical prote
38	47.5	25.3	1806	1 CGHUIE	collagen alpha 1(X
39	47	25.0	250	2 S69031	hypothetical prote
40	47	25.0	316	2 S75062	transcription regu
41	47	25.0	357	2 T38405	hypothetical prote
42	47	25.0	443	1 AJCLOA	glutamate-ammonia
43	47	25.0	468	2 B72351	clostripain-relate
44	47	25.0	502	2 T29729	hypothetical prote
45	47	25.0	571	2 S58356	pept protein - Sta

ALIGNMENTS

RESULT 1

S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009; PMID:7477296
A:Accession: S60226
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OK>
A:Cross-references: EMBL:D49949; NID:gl064822; PIDN:BAA08705.1; PID:gl064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 58.5%; Score 110; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 9.4e-08;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFVAMKFDNTLYFIAEDDENLESD 36

Db 6 EDCVNFKEMMFIDNTLYFIPENGLESD 35

RESULT 2

H71606
hypothetical protein PFB0755w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: H71606
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: H71606
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1398 <GAR>
A:Cross-references: GB:AE001416; NID:g3845268; PIDN:AAC71940.1; PID:g384
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0755w

Query Match 33.2%; Score 62.5; DB 2; Length 1398;
Best Local Similarity 31.7%; Pred. No. 2.8;
Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 4 EPVEDNCINFVAMKFI-----DNTLYFIAEDDENLESD 35

A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: G97866
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-212 <KUR>
 A:Cross-references: GB:AE006914; PIDN:AAL03873.1; PID:gl5620478; GSPDB:GN00173
 C:Genetics:
 A:Gene: RC1335

Query Match 27.9%; Score 52.5; DB 2; Length 212;
 Best Local Similarity 36.1%; Pred. No. 9.1;
 Matches 13; Conservative 5; Mismatches 7; Indels 11; Gaps 1;

QY 12 NFVAMKFID-----NTLYFTAEDDENLESD 36
 ||||| I || I: || I: I
 DB 84 NFVSMYDYDMEQVSRINRSNTFNFLEEDNEHLDDK 119

RESULT 8

T00023
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 28-Jul-2000
 C:Accession: T00023; T08879
 R:Ohira, M.; Seki, N.; Nagase, T.; Ishikawa, K.; Nomura, N.; Ohara, O.
 Genomics 47, 300-306, 1998
 A:Title: Characterization of a human homolog (BACH1) of the mouse Bach1 gene encoding a
 A:Reference number: Z14060; MUID:98140130; PMID:9479503
 A:Accession: T00023
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-736 <OHI>
 A:Cross-references: EMBL:AB002803; PIDN:BAA24932.1
 A:Experimental source: immature myeloid
 R:Blouin, J.L.; Duriaux Sail G.; Guipponi, M.; Rossier, C.; Pappasavas, M.P.; Antonarak
 Hum. Genet. 102, 282-288, 1998
 A:Title: Isolation of the human BACH1 transcription regulator gene, which maps to chromo
 A:Reference number: Z16510; MUID:98204399; PMID:9544839
 A:Accession: T08879
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-157, T', 159-170, 'G', 172-736 <BLO>
 A:Cross-references: EMBL:AF026199; MUID:92565399; PID:92565400
 C:Genetics:
 A:Gene: BACH1
 A:Map position: 21q22.1
 C:Superfamily: human transcription factor BACH1; POZ domain homology
 C:Keywords: leucine zipper; transcription factor; transcription regulation; zinc finger
 F:20-122/Domain: POZ domain homology <POZ>

Query Match 27.7%; Score 52; DB 2; Length 736;
 Best Local Similarity 31.8%; Pred. No. 39;
 Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINIVAMKFIDNT 22
 :: :||: I: ||: I:
 DB 113 LSVHNIEESCQFLKFKFLDST 134

RESULT 9

T28214
 C:Species: Melanoplus sanguinipes entomopoxvirus
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000
 C:Accession: T28214
 R:Afonso, C.D.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
 A:Reference number: Z20484; MUID:99102612; PMID:9847359
 A:Accession: T28214
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA

A:Residues: 1-647 <AFO>
 A:Cross-references: EMBL:AF063866; MUID:g4049647; PIDN:AAC97824.1; PID:g4049864
 A:Experimental source: isolate Tuscon
 C:Genetics:
 A:Note: MSV053
 C:Superfamily: vaccinia virus nucleoside-triphosphatase I
 C:Keywords: ATP; hydrolase; P-loop

Query Match 27.1%; Score 51; DB 2; Length 647;
 Best Local Similarity 31.1%; Pred. No. 47;
 Matches 14; Conservative 7; Mismatches 10; Indels 14; Gaps 1;

QY 3 AEPVEDNCI-----NFVAMKFIDNTLYFTAEDDENL 33
 ||||| I || I: || I: I:
 DB 554 AEPVENEYIFNIRTKIDVDNENNVTIKIIVSYICSEDNLNI 598

RESULT 10

T38789
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38789
 R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream Wood, V.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21811
 A:Accession: T38789
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-302 <PEA>
 A:Cross-references: EMBL:Z98560; PIDN:CAB11174.1; GSPDB:GN000066; SPDB:SPAC4C5.03
 A:Experimental source: strain 972h-; cosmid c4C5
 C:Genetics:
 A:Gene: SPDB:SPAC4C5.03
 A:Map position: 1

Query Match 26.6%; Score 50; DB 2; Length 302;
 Best Local Similarity 34.8%; Pred. No. 29;
 Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 10 CINFAMKFFIDNTLYFTAEDDEN 32
 I: : : : : I: ||||
 DB 115 CVLMFWMFLPRPIHFVAADEN 137

RESULT 11

A56590
 C:Species: Chironomus tentans
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Sep-1999
 C:Accession: A56590
 R:Imhof, M.O.; Rusconi, S.; Lezzi, M.
 Insect Biochem. Mol. Biol. 23, 115-124, 1993
 A:Title: Cloning of a Chironomus tentans cDNA encoding a protein (cEcrH) homologous
 A:Reference number: A56590; MUID:93250857; PMID:8485513
 A:Accession: A56590
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-536 <IMH>
 A:Cross-references: GB:S60739; MUID:9385993; PIDN:AAC60500.1; PID:g385894
 A:Note: sequence extracted from NCBI backbone (NCBIN:132124, NCBIP:132127)
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; steroid hormone receptor; zinc finger
 F:113-432/Domain: erba transforming protein homology <ERBA>

Query Match 26.6%; Score 50; DB 2; Length 536;
 Best Local Similarity 38.5%; Pred. No. 53;
 Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 11 INFVAMKFIDNTLYFTAEDDENLESD 36
 :||: :||: I: ||||
 DB 16 LNYASOSFGDNNIYGATKKQRLESD 41

RESULT 12

AE2254
hypothetical protein alr3588 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AE2254
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2254
A:Status: preliminary.
A:Molecule type: DNA
A:Residues: 1-908 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075287.1; PID:g17132721; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3588

Query Match 26.6%; Score 50; DB 2; Length 908;
Best Local Similarity 72.7%; Pred. No. 93;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 19 IDNLYFTAE 29
:|||||:|
Db 795 VDNTLYEVAND 805

RESULT 13

T16604
hypothetical protein K10B2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16604
R:Miller, N.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid K10B2.
A:Reference number: Z18545
A:Accession: T16604
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1009 <ML>
A:Cross-references: EMBL:U28730; MID:g860694; PID:g860699; PIDN:AAA68262.1; GSP:K10B2.5
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K10B2.5
A:Introns: 29/3; 126/1; 175/2; 226/2; 266/1; 328/2; 389/2; 527/3; 732/1; 790/3; 982/2

Query Match 26.3%; Score 49.5; DB 2; Length 1009;
Best Local Similarity 37.5%; Pred. No. 11; 2e+02;
Matches 12; Conservative 6; Mismatches 11; Indels 3; Gaps 1;
QY 3 AEPVEDNCINFAVKFIDNTLYFTAEEDNLE 34
:|||||:| |||: |||:|
Db 109 SEPQDNEKEVTTNFIDDSM---IEDHEEYE 137

RESULT 14

E97088
beta-xylosidase, family 43 glycosyl hydrolase CAC1529 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: E97088
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97088
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79496.1; PID:g15024478; GSPDB:GN00168
A:Experimental source: clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1529
C:Superfamily: Streptomyces chartreusis alpha-L-arabinofuranosidase II
Query Match 26.1%; Score 49; DB 2; Length 327;
Best Local Similarity 32.6%; Pred. No. 44;
Matches 15; Conservative 6; Mismatches 13; Indels 12; Gaps 2;
QY 3 AEPVE-----DNCINFAVKFIDNT--LYFIAEDDENLESD 36
:|||||:| |||: |||:|
Db 53 AEPVDVWRRHESGEMSLIWAPEIHFINGAWYIVFAAAPDKNIEDD 98

RESULT 15
A82890
hypothetical protein U0451 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82890
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
A:Reference number: A82870
A:Accession: A82890
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <GLA>
A:Cross-references: GB:AE002141; GB:AF222894; MID:g6899434; PIDN:AAF30863.1; GSPDB:GN001437
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: U0451
A:Genetic code: SGC3
Query Match 26.1%; Score 49; DB 2; Length 338;
Best Local Similarity 32.4%; Pred. No. 45;
Matches 11; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
QY 3 AEPVEDNCINFAVKFIDNTLYFTAEEDDENLESD 36
:|||||:| |||: |||:|
Db 225 AOLVYDECLLAPOSSVFPNNEYFIEEVEYEHIDPD 258

Search completed: April 23, 2003, 08:20:39
Job time : 46 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 11 seconds
(without alignments)
135.741 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMKFDNTLYFAIEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	188	100.0	193	1	1	IL18_HUMAN	Q14116 homo sapien
2	159	84.6	193	1	1	IL18_HORSE	Q9xsq7 equus cabal
3	147.5	78.5	192	1	1	IL18_PIG	O19073 bos scrofa
4	146	77.7	193	1	1	IL18_BOVIN	Q9tu73 sus taurus
5	136	72.3	193	1	1	IL18_CANFA	Q9xsr0 canis famil
6	110	58.5	192	1	1	IL18_MOUSE	P70380 mus musculu
7	109	58.0	194	1	1	IL18_RAT	P97636 rattus norv
8	55	29.3	688	1	1	CACM_YEAST	P80235 saccharomyc
9	52.5	27.9	183	1	1	LGUL_MOUSE	Q9cpu0 mus musculu
10	52	27.7	736	1	1	BAC1_HUMAN	O14867 homo sapien
11	52	27.7	739	1	1	BAC1_MOUSE	P97302 mus musculu
12	51	27.1	647	1	1	NTP1_MSEPV	Q9vw39 melanoplus
13	50	26.6	302	1	1	YDX3_SCHPO	O14166 schizosacch
14	50	26.6	536	1	1	ECR_CHITE	P49882 chironomus
15	49	26.1	776	1	1	VP41_ROTST	P04508 smian il r
16	49	26.1	776	1	1	VP41_ROTBC	P08713 bovine rota
17	49	26.1	776	1	1	VP4_ROTST	P17463 simian il r
18	49	26.1	1628	1	1	YABE_SCHPO	Q09779 schizosacch
19	48.5	25.8	299	1	1	SUT1_YEAST	P53032 saccharomyc
20	48.5	25.8	464	1	1	VGIL_AMEPV	P29817 ansacta moo
21	48.5	25.8	855	1	1	GCFC_MOUSE	P58501 mus musculu
22	48.5	25.8	3712	1	1	LMA_DROME	Q00174 drosophila
23	47.5	25.3	482	1	1	CA1B_RAT	P20909 rattus norv
24	47.5	25.3	1435	1	1	DPO3_MYCPU	P47729 mycoplasma
25	47.5	25.3	1806	1	1	CA1B_HUMAN	P12107 homo sapien
26	47	25.0	357	1	1	YFQB_SCHPO	Q10170 schizosacch
27	47	25.0	443	1	1	GLNA_CLOSA	P10656 clostridium
28	47	25.0	690	1	1	ATM1_YEAST	P40416 saccharomyc
29	47	25.0	774	1	1	VP4_ROTHT	P11200 human rotav
30	47	25.0	775	1	1	VP4_ROTHT	P11197 human rotav
31	47	25.0	776	1	1	VP4_ROTHT	P36305 bovine rota
32	47	25.0	776	1	1	VP4_ROTHT	P11199 human rotav
33	47	25.0	2146	1	1	INSR_DROME	P09208 drosophila

34 46.5 24.7 232 1 YEJ0_YEAST
35 46.5 24.7 321 1 YH28_YEAST
36 46.5 24.7 390 1 Y109_NPVAC
37 46.5 24.7 549 1 SYR_ARCFU
38 46.5 24.7 818 1 SAP4_YEAST
39 46.5 24.7 249 1 YS87_CAEEL
40 46 24.5 368 1 YR2_HPV45
41 46 24.5 618 1 YKR4_YEAST
42 46 24.5 917 1 GCFC_HUMAN
43 46 24.5 1170 1 ITAL_HUMAN
44 46 24.5 3396 1 PCGV_HUMAN
45 45.5 24.2 183 1 LGUL_HUMAN

ALIGNMENTS

RESULT 1
IL18_HUMAN
ID IL18_HUMAN STANDARD: PRT: 193 AA.
AC Q14116; 075599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
in Escherichia coli, and studies on the biologic activities of the
protein".
RT J. Immunol. 156:4274-4279(1996).
RL [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18".
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA".
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=Urinary bladder;
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL [5]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=Peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; D49950; BAA08706.1;
 DR EMBL; AF077611; AAC27787.1;
 DR EMBL; AY044641; AAK95950.1;
 DR EMBL; BC007007; AAH07007.1;
 DR EMBL; BC007461; AAH07461.1;
 DR EMBL; U90434; AAB50010.1;
 DR Genew; HGNC:5986; IL18.
 DR MIN; 600953;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.

FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 100.0%; Score 188; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36

RESULT 2
 IL18_HORSE
 ID IL18_HORSE STANDARD; PRT; 193 AA.
 AC QX507;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
 Argyle D.J., Onions D.E.,
 "Nucleotide sequence of equine interleukin 12 and 18 cDNAs."
 Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; Y11131; CAA72013.1;
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 84.6%; Score 159; DB 1; Length 193;
 Best Local Similarity 83.3%; Pred. No. 1.3e-15;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36

RESULT 3
 IL18_PIG
 ID IL18_PIG STANDARD; PRT; 192 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (IFN-gamma-18 precursor (IL-18) (interferon-gamma inducing factor))
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 35

RESULT 4
 IL18_BOVIN
 ID IL18_BOVIN STANDARD; PRT; 193 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (IFN-gamma-18 precursor (IL-18) (interferon-gamma inducing factor))
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 35

RESULT 4
 IL18_BOVIN
 ID IL18_BOVIN STANDARD; PRT; 193 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (IFN-gamma-18 precursor (IL-18) (interferon-gamma inducing factor))
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 35

RESULT 4
 IL18_BOVIN
 ID IL18_BOVIN STANDARD; PRT; 193 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (IFN-gamma-18 precursor (IL-18) (interferon-gamma inducing factor))
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 35

RESULT 4
 IL18_BOVIN
 ID IL18_BOVIN STANDARD; PRT; 193 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (IFN-gamma-18 precursor (IL-18) (interferon-gamma inducing factor))
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Foss D.L., Murtaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

OY 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 36
 |||||
 Db 1 MAAPVEDNCINFVAMKFIQNTLYFIAEDDENLESD 35


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FT: CONFLICT 148 48 11-->M (IN REF. 2).
SQ: SEQUENCE 194 AA: 22303 MW: E2089ADGFI1798450 CRC64;

Query Match
Best Local Similarity 58.0%; Score 109.; DB I; Length 194;
Query Local Similarity 61.1%; Pred. No. 1.9e-08;
Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY: 1 MAAPEDVNCINFVMKFDINTLYTFAEDDENLESD 36
    III :||| :||||| ||: ||||
DB: 1 MAAMSEGGSCVNFEMFIDNTLYLIPEDNGDLES 36
    III :||| :||||| ||: ||||

RESULT 8
CACH_YEAST STANDARD; PRT; 688 AA.
AC ACACMYEAST
AC P80235;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Putative mitochondrial carnitine O-acetyltransferase (EC 2.3.1.7).
GN YAT1 OR YAR035W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DL-1.
RX MEDLINE=94086564; PubMed=8262985;
RT Schmalix W., Handlow W.;
RA "The ethanol-inducible YAT1 gene from yeast encodes a presumptive
RRL mitochondrial outer carnitine acetyltransferase.";
RRT J. Biol. Chem. 268:27428-27439(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288c / AB972;
RX MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RR Hall J., Ouellette B.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RRT Storms R.K.;
RA "The nucleotide sequence of chromosome I from Saccharomyces
RRL cerevisiae.";
RRT Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
CC -! FUNCTION: INVOLVED IN THE TRANSFER OF ACETYL-COA INTO
CC MITOCHONDRIA. MAY ALSO BE INVOLVED IN THE METABOLISM OF ACETATE
CC AND OF ETHANOL.
CC -! CATALYTIC ACTIVITY: Acetyl-CoA + carnitine = CoA + O-
CC acetylcarnitine.
CC -! PATHWAY: SECOND STEP IN TRANSPORT OF FATTY ACIDS INTO
CC MITOCHONDRIA.
CC -! SUBCELLULAR LOCATION: Mitochondrial inner membrane; outer side.
CC INDUCTION: BY ETHANOL AND BY ACETATE. REPRESSED BY GLUCOSE,
CC AND TO A LESSER EXTENT, BY GALACTOSE. DEREPRESSED BY GLYCEROL.
CC -! SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
CC FAMILY.
CC
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CC send an email to license@isb-sib.ch).
CC -----
CC EMBL; X74553; CAAS2647.1;
CC EMBL; L28920; AAC09495.1;
CC PIR; S36631; S36631;
CC PIR; S47902; S47902;
CC SCD; S0000080. YAT1;
CC InterPro; IPRO00542; Carn_acyltransf.
CC Pfam; PF00755; Carn_acyltransf; 1.
CC PROSITE; PS00439; ACYLTRANSF_C1; FALSE_NEG.
CC PROSITE; PS00440; ACYLTRANSF_C2; 1.

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EMBL; AK002386; BAB22060.1; -
EMBL; AK003567; BAB22863.1; -
EMBL; AK005055; BAB23781.1; -
HSSP; Q04760; IQIP.
MGD; MGI:95742; Glol.
InterPro: IPR004361; Glyoxalase_1.
InterPro: IPR004360; Gly_bleo_diox.
Pfam: PF00903; Glyoxalase_1.
ProDom: PD002334; Glyoxalase_1.
TIGRFRAMS; TIGR00068; glyox_I; 1.
PROSITE; PS00934; GLYOXALASE_1; 1.
PROSITE; PS00935; GLYOXALASE_1_2; 1.
Lyase; Zinc.
INIT_MET 0 0 BY SIMILARITY.
METAL 33 33 ZINC (BY SIMILARITY).
METAL 99 99 ZINC (BY SIMILARITY).
METAL 126 126 ZINC (BY SIMILARITY).
METAL 172 172 ZINC (BY SIMILARITY).
SEQUENCE 183 AA; 20678 MW; 8B9EFOAID845002C CRC64;

Query Match 27.9%; Score 52.5; DB 1; Length 183;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 11; Conservative 6; Mismatches 2; Indels 3; Gaps 1;

yy 11 INFVAMKFDINTLYFFIAEDDEN 32
::| | | | : | | | : | | : | |
bb 60 LDPFAMKF---SLYFLAYEDKN 78

RESULT 10
WACL_HUMAN STANDARD; PRT: 736 AA.
D BACL_HUMAN
AC OI4867; O43285;
15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription regulator protein BACH1 (BTB and CNC homolog 1)
(HA2303).
BACH1.
Homo sapiens (Human).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
MEDLINE=98204399; PubMed=9544839;
Blouin J.-L., Durlaux Sall G., Guipponi M., Rossier C.,
Pappasavas M.-P., Antonarakis S.E.;
"Isolation of the human BACH1 transcription regulator gene, which
maps to chromosome 21q22.1.";
Hum. Genet. 102:282-288(1998).
[2]
SEQUENCE FROM N.A.
MEDLINE=98140130; PubMed=9479503;
Ohira M., Seki N., Nagase T., Ishikawa K., Nomura N., Ohara O.;
"Characterization of a human homolog (BACH1) of the mouse Bach1 gene
encoding a BTB-basic leucine zipper transcription factor and its
mapping to chromosome 21q22.1.";
Genomics 47:300-306(1998).
[3]
SEQUENCE FROM N.A.
Taudien S., Dagand E., Delabar J., Nordstiek G., Drescher B., Weber J.,
Schattvey R., Yaspo M.-L., Rosenthal A.;
Submitted (JAN-1999) to the EMBL/GenBank/DBS databases.
[4]
SEQUENCE FROM N.A.
MEDLINE=20289799; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

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OX NCBI_TaxID=83191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tucson;
 RX MEDLINE=99102612; PubMed=9847359;
 RA Alfonso C.L., Tulman-E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RT "The genome of Melanoplus sanguinipes entomopoxvirus";
 RL J. Virol. 73:533-552(1999).
 CC -!- FUNCTION: SERVES TWO ROLES IN TRANSCRIPTION: IT ACTS IN CONCERT
 CC WITH VIRAL TERMINATION FACTOR/CAPPING ENZYME TO CATALYZE RELEASE
 CC OF UUUUUU-CONTAINING NASCENT RNA FROM THE ELONGATION COMPLEX, AND
 CC IT ACTS BY ITSELF AS A POLYMERASE ELONGATION FACTOR TO FACILITATE
 CC TRANSCRIPTION OF INTRINSIC PAUSE SITES (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
 CC -!- SIMILARITY: BELONGS TO THE NPH 1 SUBFAMILY OF HELICASES.
 CC
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 CC
 CC EMBL: AF063866; AAC97824.1; -;
 CC InterPro: IPR001650; Helicase_C.
 CC InterPro: IPR00330; SNF2_N.
 CC Pfam: PF00176; SNF2_N; 1.
 CC Pfam: PF00271; Helicase_C; 1.
 CC SMART: SM00490; HELIC; 1.
 CC Hydrolase; ATP-binding; Transcription.
 CC KW DOMAIN 40 322 SNF2_N.
 CC FT DOMAIN 404 490 HELICASE_C.
 CC FT NP_BIND 61 68 ATP (BY SIMILARITY).
 CC FT SITE 150 153 DEXH BOX
 CC SQ SEQUENCE 647 AA; 75134 MW; E78C7F768235D51D CRC64;
 Query Match 27.1%; Score 51; DB 1; Length 647;
 Best Local Similarity 31.1%; Pred. No. 15;
 Matches 14; Conservative 7; Mismatches 10; Indels 14; Gaps 1;
 OY 3 APVEDNCI-----NFVAMKFIDNTLYFIAEDDENL 33
 DB 554 APPEVNEYIFNRIKIDVDNENNVITKIIVSPIYCSEDNLI 598
 RESULT 13
 YDX3_SCHPO STANDARD; PRT; 302 AA.
 ID YDX3_SCHPO
 AC O14166;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C4C5.03 in chromosome I.
 GN SPAC4C5.03.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Besham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares S., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Carlson A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe";
 RL Nature 415:871-880(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC
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 CC
 CC EMBL: Z98560; CAB11174.1;
 CC KW Hypothetical protein; Transmembrane.
 CC FT TRANSMEM 25 45 POTENTIAL.
 CC FT TRANSMEM 58 78 POTENTIAL.
 CC FT TRANSMEM 104 124 POTENTIAL.
 CC FT TRANSMEM 158 178 POTENTIAL.
 CC FT TRANSMEM 182 202 POTENTIAL.
 CC FT TRANSMEM 215 235 POTENTIAL.
 CC FT TRANSMEM 247 267 POTENTIAL.
 CC SQ SEQUENCE 302 AA; 33854 MW; 0D7D7AB3D21E3C12 CRC64;
 Query Match 26.6%; Score 50; DB 1; Length 302;
 Best Local Similarity 34.8%; Pred. No. 8;
 Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 OY 10 CINFVAMKFIDNTLYFIAEDDEN 32
 DB 115 CVMFAMFELPRPHFVAADDEN 137
 RESULT 14
 ECR_CHITE STANDARD; PRT; 536 AA
 ID ECR_CHITE
 AC P49882;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
 DE receptor) (20E receptor) (ECRH).
 GN ECR OR NR1H1.
 OS Chironomus tentans (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93250857; PubMed=8485513;
 RA Imhof M.O., Rusconi S., Lezzi M.;
 RT "Cloning of a Chironomus tentans cDNA encoding a protein (cECRH)
 RT homologous to the Drosophila melanogaster ecdysteroid receptor
 RT (dECR).";
 RL Insect Biochem. Mol. Biol. 23:115-124(1993).
 CC -!- FUNCTION: RECEPTOR FOR ECDYSONE. BINDS TO ECDYSONE RESPONSE
 CC ELEMENTS (ECRES).
 CC -!- SUBCELLULAR LOCATION: Nuclear.

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	188	100.0	193	4	Q96KJ8	Q96KJ8 homo sapien
2	179	95.2	193	6	Q9BG15	Q9BG15 macaca mula
3	155	82.4	193	6	Q9GL09	Q9GL09 oviss aries
4	147.5	78.5	192	6	Q9N1P7	Q9N1P7 sus scrofa
5	143.5	76.3	192	6	Q95W33	Q95W33 felis silve
6	110	58.5	196	11	Q91Z66	Q91Z66 sigmondon hi
7	93	49.5	178	6	Q9MZL8	Q9MZL8 bos taurus
8	62.5	33.2	1398	5	Q96244	Q96244 plasmodium
9	55	29.3	275	16	Q99TA3	Q99TA3 staphylococ
10	54	28.7	417	5	Q96410	Q96410 hydra atten
11	53.5	28.5	1055	12	Q65146	Q65146 african swi
12	53	28.2	70	2	Q9JN03	Q9JN03 campylobact
13	53	28.2	365	16	Q9PNP3	Q9PNP3 campylobact
14	53	28.2	1039	5	Q9GV97	Q9GV97 toxoplasma
15	52.5	27.9	149	11	Q9DB53	Q9DB53 mus musculu
16	52.5	27.9	184	11	O8R3T1	O8R3T1 mus musculu

OS	Sus scrofa (pig)	
OC	Eukaryota: Metazoa	
OC	Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus	
OX	NCBI_TaxID=9823;	
	[1]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=LUNG	
RC		

Query Match 58.5%; Score 110; DB 11; Length 196;
Best Local Similarity 63.9%; Pred. No. 9; 1e-08;

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrett B.G.,
 RT "the genome sequence of the food-borne pathogen *Campylobacter jejuni*
 RT reveals hypervariable sequences";
 RL Nature 403:665-668(2000).
 DR EMBL: AL139077; CAB73304.1; -
 DR InterPro: IPR001261; ARGE-DAPE_CPG2.
 DR InterPro: IPR002933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 DR TIGRFAMS: TIGR01246; daPE_protoc; 1.
 DR PROSITE: PS00758; ARGE-DAPE_CPG2_1; UNKNOWN_1.
 KW Complete proteome
 SQ SEQUENCE 365 AA; 40457 MW; AE85159CDF09CB7E CRC64;
 Query Match 281%; Score 53; DB 16; Length 365;
 Best Local Similarity 361%; Pred. No. 22;
 Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 5 PVEDNCINFAVAKFIDNTLYFAED 29
 Db 18 PNDGALNFTAMELSDFEAFFIEKE 42
 RESULT 14
 Q9GV97 PRELIMINARY; PRT; 1039 AA.
 AC Q9GV97
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Plasma-membrane H⁺-ATPase.
 GN PMAL
 OS Tokoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
 OC Tokoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P-STRAIN;
 RX MEDLINE=21126593; PubMed=11223136;
 RA Holpert M., Lueder C.G.K., Gross U., Bohne W.,
 RT "Bradyzoite-specific expression of a P-type ATPase in *Toxoplasma*
 RT gondii";
 RL Mol. Biochem. Parasitol. 112:293-296(2001).
 DR EMBL: AJ278874; CAC05676.1; -
 DR InterPro: IPR001757; ATPase_E1-E2.
 DR InterPro: IPR004014; Cation_ATPase.
 DR InterPro: IPR001454; Hignase/hydrilase.
 DR Pfam: PF00690; Cation_ATPase.N; 1.
 DR Pfam: PF00122; E1-E2_ATPase; 1.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PRINTS: PR00119; CATAPASE.
 DR PRINTS: PR00120; HATPASE.
 DR PROSITE: PS00154; ATPASE_E1-E2; UNKNOWN_1.
 SQ SEQUENCE 1039 AA; 115658 MW; DAA52C61B7FFAB14 CRC64;

Query Match 28.2%; Score 53; DB 5; Length 1039;
 Best Local Similarity 43.5%; Pred. No. 62;
 Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 12 NFVAMKFIIDNTLYFAEDNLE 34
 Db 895 NNASKVMQNTVHLEERENVE 917

RESULT 15
 Q9DB53 PRELIMINARY; PRT; 149 AA.
 ID Q9DB53
 AC Q9DB53;

DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 1110008E19RIK protein;
 GN 1110008E19RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RT Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK005215; BAB23888.1;
 DR HSSP: Q04760; IOIP.
 DR MGD: MGI:1913383; 1110008E19RIK.
 DR InterPro: IPR004361; Glyoxalase_1.
 DR InterPro: IPR004360; Gly-bleo_diox.
 DR Pfam: PF00903; Glyoxalase; 1.
 DR PRODOM: PD002334; Glyoxalase_1; 1.
 DR TIGRFAMS: TIGR00068; glyox_I; 1.
 DR PROSITE: PS00935; GLYOXALASE_I_2; 1.
 SQ SEQUENCE 149 AA; 17036 MW; 5CAF060B831D1B82 CRC64;
 Query Match 27.9%; Score 52.5; DB 11; Length 149;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 11; Conservative 6; Mismatches 2; Indels 3; Gaps 1;
 QY 11 INFVAMKFIIDNTLYFAEDDEN 32
 Db 26 LDFFAMKF---SLYFLAYEDKN 44

Search completed: April 23, 2003, 08:18:14
 Job time : 88 secs

Devil, S.
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FILE 'REGISTRY' ENTERED AT 10:29:52 ON 23 APR 2003
L1 15 S MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD/SQSP

FILE 'HCAPLUS' ENTERED AT 10:31:01 ON 23 APR 2003
L2 13 S L1

L2 ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:55562 HCAPLUS

DOCUMENT NUMBER: 138:84318

TITLE: Generation and initial analysis of more than
15,000 full-length human and mouse cDNA
sequences

AUTHOR(S): Strausberg, Robert L.; Feingold, Elise A.;
Grouse, Lynette H.; Derge, Jeffery G.; Klausner,
Richard D.; Collins, Francis S.; Wagner, Lukas;
Shenmen, Carolyn M.; Schuler, Gregory D.;
Altschul, Stephen F.; Zeeberg, Barry; Buetow,
Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.;
Hopkins, Ralph F.; Jordan, Heather; Moore, Troy;
Max, Steve I.; Wang, Jun; Hsieh, Florence;
Diatchenko, Luda; Marusina, Kate; Farmer, Andrew
A.; Rubin, Gerald M.; Hong, Ling; Stapleton,
Mark; Soares, M. Bento; Bonaldo, Maria F.;
Casavant, Tom L.; Scheetz, Todd E.; Brownstein,
Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki;
Carninci, Piero; Prange, Christa; Raha, Sam S.;
Loquellano, Naomi A.; Peters, Garrick J.;
Abramson, Rick D.; Mullahy, Sara J.; Bosak,
Stephanie A.; McEwan, Paul J.; McKernan, Kevin
J.; Malek, Joel A.; Gunaratne, Preethi H.;
Richards, Stephen; Worley, Kim C.; Hale, Sarah;
Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen
W.; Villalon, Debbie K.; Muzny, Donna M.;
Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard
A.; Fahey, Jessica; Helton, Erin; Kettelman,
Mark; Madan, Anuradha; Rodrigues, Stephanie;
Sanchez, Amy; Whiting, Michelle; Madan, Anup;
Young, Alice C.; Shevchenko, Yuriy; Bouffard,
Gerard G.; Blakesley, Robert W.; Touchman,
Jeffrey W.; Green, Eric D.; Dickson, Mark C.;
Rodriguez, Alex C.; Grimwood, Jane; Schmutz,
Jeremy; Myers, Richard M.; Butterfield, Yaron S.
N.; Krzywinski, Martin I.; Skalska, Ursula;
Smailus, Duane E.; Schnerch, Angelique; Schein,
Jacqueline E.; Jones, Steven J. M.; Marra, Marco
A.

CORPORATE SOURCE: National Cancer Institute, NIH, Bethesda, MD,
20892-2580, USA

SOURCE: Proceedings of the National Academy of Sciences
of the United States of America (2002), 99(26),
16899-16903

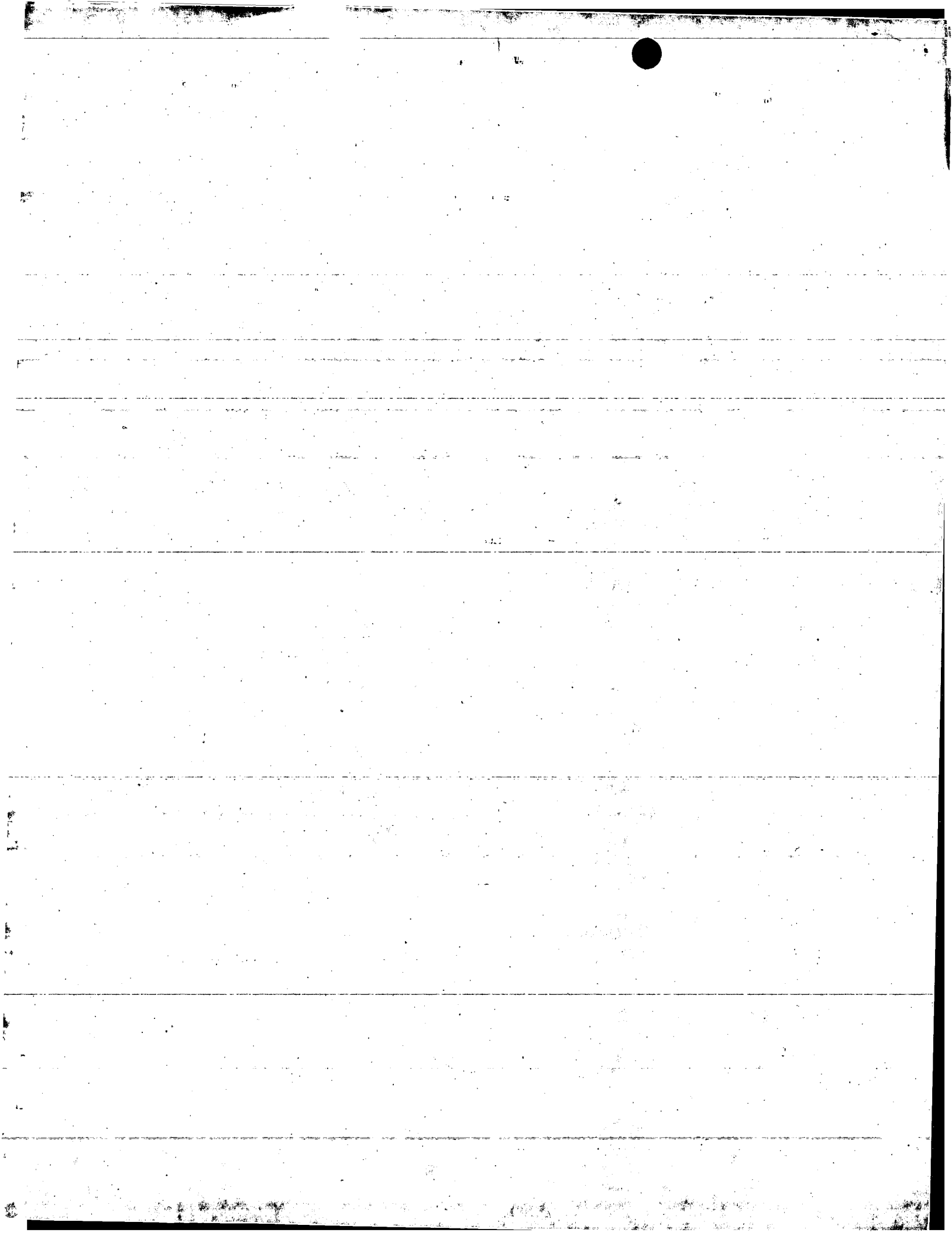
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The National Institutes of Health Mammalian Gene Collection (MGC)
Program is a multiinstitutional effort to identify and sequence a
cDNA clone contg. a complete ORF for each human and mouse gene.



09/711896

ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstr. record is one of eleven records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT 480762-83-2, GenBank AAH07007 480765-89-7

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)

L2 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:935747 HCAPLUS

DOCUMENT NUMBER: 136:68716

TITLE: Method for preparing a physiologically active IL-18 polypeptide

INVENTOR(S): Johanson, Kyung O.; Kirkpatrick, Robert B.; Shatzman, Allan R.; Ho, Yen Sen; McDevitt, Patrick

PATENT ASSIGNEE(S): Smithkline Beecham Corporation, USA

SOURCE: PCT Int. Appl., 64 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001098455	A2	20011227	WO 2001-US18804	20010611
WO 2001098455	A3	20020808		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 2001080442	A5	20020102	AU 2001-80442	20010611
EP 1292697	A2	20030319	EP 2001-958830	20010611
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			

PRIORITY APPLN. INFO.:

US 2000-211832P P 20000615
US 2000-224128P P 20000810
US 2001-264923P P 20010120
WO 2001-US18804 W 20010611

AB A method for producing a physiol. active polypeptide, comprising contacting a precursor polypeptide with an activating enzyme, or

09/711896

co-expressing the polypeptide with an activating protease. The method is useful for inducing interferon .gamma. prodn. in immunocompetent cells, enhancing killing activity of NK cells, and promoting differentiation of naive CD4+ T cell into Th1 cells.

IT 383927-79-5P, Interleukin 18 (human precursor)
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; activation of IL-18 by contacting or co-expressing precursor IL-18 with an activating protease)

L2 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:693554 HCAPLUS

DOCUMENT NUMBER: 135:271914

TITLE: Treatment of allergies using an IL-18-antigen fusion protein

INVENTOR(S): Levy, Shoshana; Dekruffy, Rosemarie H.; Umetsu, Dale T.; Maecker, Holden

PATENT ASSIGNEE(S): Board of Trustees of the Leland Stanford Junior University, USA

SOURCE: PCT Int. Appl., 38 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001068896	A1	20010920	WO 2001-US6869	20010302
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
US 2001044418	A1	20011122	US 2001-798075	20010302
PRIORITY APPLN. INFO.:		US 2000-188311P P 20000310		
AB	Allergic and other immune disorders assocd. with antigen specific T cells are treated by administering a vaccine comprising sequences of a fusion protein of IL-18 and antigen. The methods are particularly useful in decreasing an established antigen specific IgE immune response. Conditions of particular interest include asthma, allergic rhinitis, IgE-mediated anaphylactic reactions to insect stings, and other allergic conditions.			
IT	178234-94-1, Interleukin 18 (human precursor)			
	RL: PRP (Properties) (unclaimed protein sequence; treatment of allergies using an IL-18-antigen fusion protein)			
REFERENCE COUNT:	5	THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT		

L2 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:376807 HCAPLUS

DOCUMENT NUMBER: 135:4468

TITLE: Antibody specific to interleukin 18 precursor

INVENTOR(S): Tohru, Kayano; Taniguchi, Mutsuko; Yamauchi, Hiroshi; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo, Japan

09/711896

SOURCE: Eur. Pat. Appl., 27 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1101772	A1	20010523	EP 2000-310121	20001115
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001204466	A2	20010731	JP 2000-349160	20001116
PRIORITY APPLN. INFO.: JP 1999-324860 A 19991116				
AB	Disclosed are an antibody specific to interleukin 18 (IL-18) precursor, prepn. processes therefor, and uses thereof. The antibody includes Igs in both forms of polyclonal and monoclonal antibodies which exhibits an immunoreactivity against IL-18 precursor at an intensity higher than against other substances. The antibody is useful in detection and purifn. of IL-18 precursor and in elimination and detoxification of the precursor accumulated in vivo. The detection method using the antibody is effective in qual. and quant. analyses for the precursor as well as in correction of imprecise results caused by assays using anti-IL-18 antibody which exhibits a cross reactivity against the precursor.			
IT	178254-43-8 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence; antibody specific to interleukin 18 precursor for treating autoimmune disease)			
IT	341990-01-0 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (antibody specific to interleukin 18 precursor for treating autoimmune disease)			
REFERENCE COUNT:	8	THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT		

L2 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:774182 HCAPLUS
DOCUMENT NUMBER: 132:277966
TITLE: Cloning and expression of precursor and mature human interleukin-18 in Escherichia coli
AUTHOR(S): Du, Yong; Wang, Tao; Du, Guixin; Xu, Jing; Hou, Lihua; Wang, Haitao
CORPORATE SOURCE: Department of Applied Molecular Biology, Beijing Institute of Microbiology and Epidemiology, Beijing, 100071, Peop. Rep. China
SOURCE: Mianyxue Zazhi (1999), 15(4), 226-228
CODEN: MIZAED; ISSN: 1000-8861
PUBLISHER: Mianyxue Zazhi Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB The cDNAs encoding precursor and mature human interleukin-18 was amplified from total RNA of a hepatitis C virus carrier's peripheral blood mononuclear cells (PBMC) by RT-PCR resp. Two recombinant plasmids pQEIL18p and pQEIL18m were constructed by cloning cDNA of

09/711896

IL-18m into pQE-30 vector. The E. coli M15 harboring the two kinds of constructs expressed recombinant proteins with mol. wt. 24 KD and 19 KD, resp. by induction of IPTG. Both proteins were purified with Nickel chelate affinity chromatog. The recombinant mature IL-18 induced INF-.gamma. prodn. of Con A-stimulated PBMC.

IT 263886-60-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning and expression of precursor and mature human interleukin-18 in Escherichia coli)

L2 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:133621 HCAPLUS

DOCUMENT NUMBER: 128:166370

TITLE: Preparation of an interferon-gamma inducing polypeptide

INVENTOR(S): Tanimoto, Tadao; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 18 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 821005	A2	19980128	EP 1997-305376	19970718
EP 821005	A3	19991013		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 5891663	A	19990406	US 1997-896501	19970718
JP 10271998	A2	19981013	JP 1997-213885	19970725
PRIORITY APPLN. INFO.:			JP 1996-213267	19960725
			JP 1997-31474	19970131

AB A method for converting a precursor of a polypeptide that induces IFN-.gamma. prodn. in immunocompetent cells, characterized in that it comprises a step of contacting an interleukin-1.beta. converting enzyme with the precursor to convert it into an active polypeptide that induces IFN-.gamma. prodn. in immunocompetent cells. PRCHuGF contg. precursor polypeptide and pCDHICE encoding interleukin 1.beta.-converting enzyme were prepd., and active polypeptide contg. Tyr-Phe-Gly-Lys-Leu at the N-terminal region was purified for inducing prodn. of interferon .gamma..

IT 178234-94-1, Interleukin 18 (human) 202608-43-3

RL: PRP (Properties)

(amino acid sequence; prepn. of .gamma. interferon prodn.-inducing polypeptide and interleukin 1.beta.-converting enzyme)

IT 202538-32-7P

RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of .gamma. interferon prodn.-inducing polypeptide and interleukin 1.beta.-converting enzyme)

09/711896

L2 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:133533 HCAPLUS

DOCUMENT NUMBER: 128:151108

TITLE: Enzyme which activates an interferon-.gamma.
inducing polypeptide

INVENTOR(S): Tanimoto, Tadao; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 18 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 819757	A2	19980121	EP 1997-305377	19970718
EP 819757	A3	19991013		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10080270	A2	19980331	JP 1997-156062	19970530
TW 480285	B	20020321	TW 1997-86110174	19970717
US 5879942	A	19990309	US 1997-896605	19970718
PRIORITY APPLN. INFO.:			JP 1996-207691	A 19960719
			JP 1997-156062	A 19970530

AB An enzyme or a protein is disclosed which converts a precursor of a polypeptide that induces IFN-.gamma. prodn. in an immunocompetent cell into the active form. The enzyme is produced from proliferating cells (THP-1, U-939, or HL-60 cells) and purified by (NH4)2SO4 pptn., and chromatog. on DEAD 5PW, S-Sepharose, Mono S, and Superdex 200 columns. The enzyme activates the INF-.gamma.-inducing precursor protein by cleavage of the bond between Asp36 and Tyr37, has a mol. wt. of about 25,000 Da and about 10,000 Da on SDS-PAGE, and is inhibited by iodoacetamide and Ac-YVAD-CHO. Partial amino acid sequences are provided for peptide fragments of the enzyme.

IT 178234-94-1, Interleukin 18 (human) 202538-32-7
202608-43-3

RL: BPR (Biological process); BSU (Biological study, unclassified);
BIOL (Biological study); PROC (Process)
(enzyme which activates an interferon-.gamma. inducing
polypeptide)

L2 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:116142 HCAPLUS

DOCUMENT NUMBER: 128:137190

TITLE: Genomic DNA encoding a polypeptide capable of
inducing the production of interferon-.gamma.

INVENTOR(S): Okura, Takanori; Torigoe, Kakuji; Kurimoto,
Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

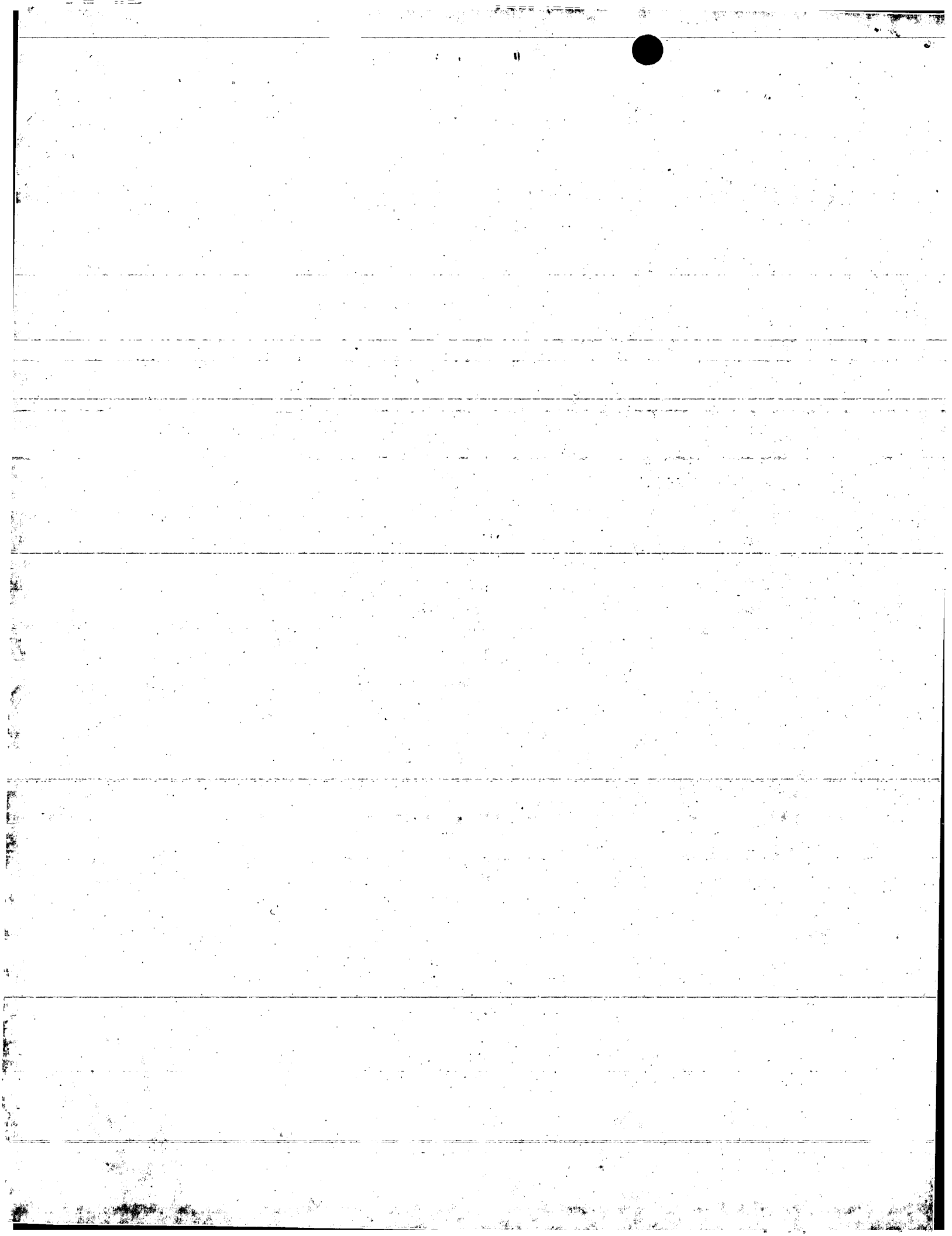
SOURCE: Eur. Pat. Appl., 74 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1



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PATENT INFORMATION:

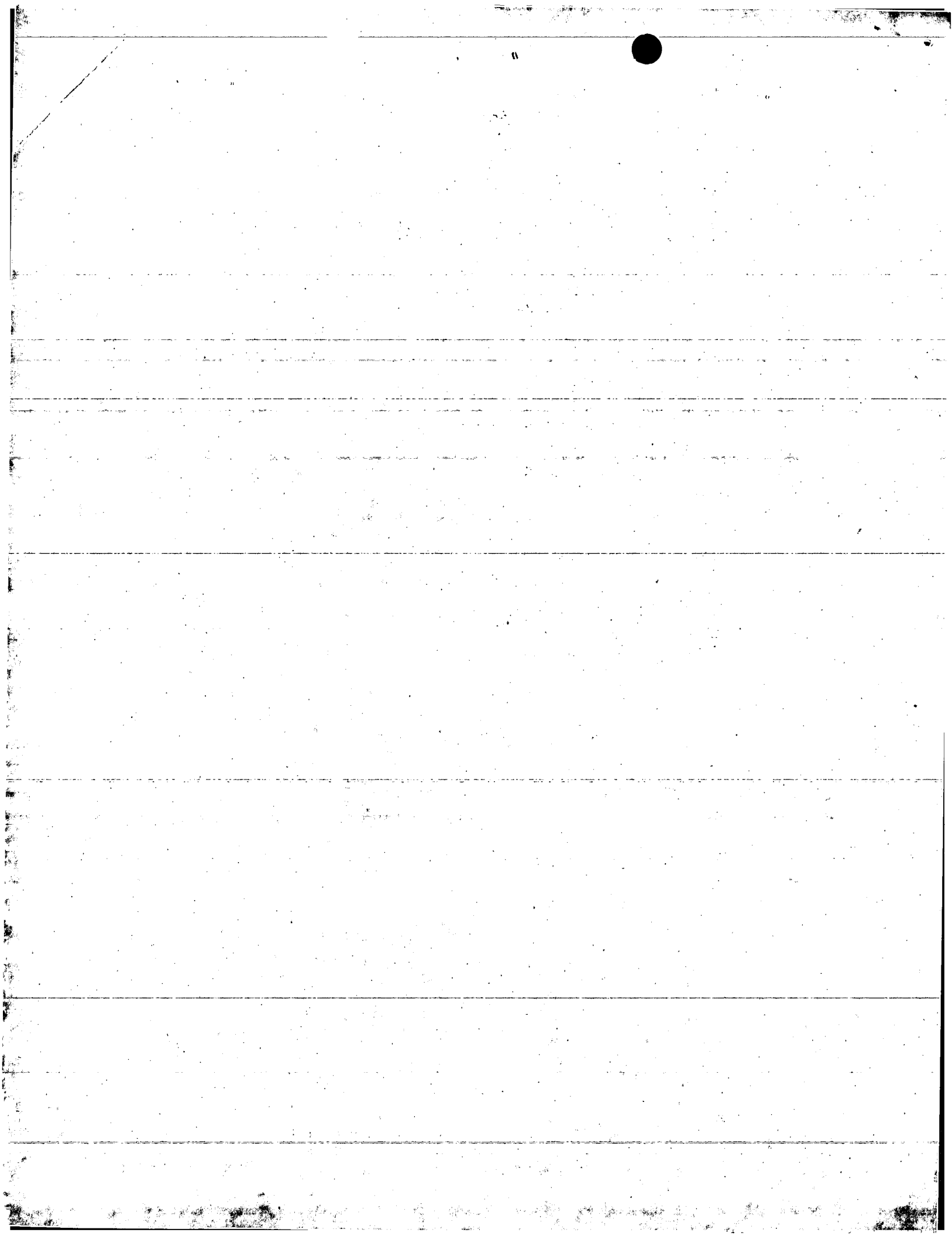
PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 816499	A2	19980107	EP 1997-304616	19970627
EP 816499	A3	19991027		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10080288	A2	19980331	JP 1997-187418	19970627
US 6060283	A	20000509	US 1997-884324	19970627
PRIORITY APPLN. INFO.:			JP 1996-185305	19960627

AB Disclosed is a human genomic DNA encoding a polypeptide capable of inducing the prodn. of interferon-.gamma. by immunocompetent cells. The gene comprises at least 5 introns and 6 exons, and a sequence of 28,994 bp was detd. for the gene, including an extensive 5'-flanking region. The genomic DNA efficiently expresses the polypeptide with high biol. activities of such as inducing the prodn. of interferon-.gamma. by immunocompetent cells, enhancing killer cells' cytotoxicity and inducing killer cells' formation, when introduced into mammalian host cells. Recombinant plasmid vectors are constructed for expression of the polypeptide in Escherichia coli and CHO cells. The high biol. activities of the polypeptide facilitate its uses to treat and/or prevent malignant tumors, viral diseases, bacterial infectious diseases and immune diseases without serious side effects when administered to humans.

IT **178254-43-8P**
 RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (amino acid sequence; genomic DNA encoding a polypeptide capable of inducing the prodn. of interferon-.gamma.)

L2 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 1997:776271 HCAPLUS
 DOCUMENT NUMBER: 128:58316
 TITLE: Human interleukin-1.gamma. and antagonists thereof
 INVENTOR(S): Sana, Theodore R.; Timans, Jacqueline C.; Hardiman, Gerard T.; Kastelein, Robert A.; Bazan, J. Fernando
 PATENT ASSIGNEE(S): Schering Corporation, USA
 SOURCE: PCT Int. Appl., 62 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9744468	A1	19971127	WO 1997-US7282	19970516
W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CZ, EE, GE, HU, IL, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				



09/711896

AU 9731166 A1 19971209 AU 1997-31166 19970516
EP 914453 A1 19990512 EP 1997-926391 19970516
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT,
IE, LT, LV, FI, RO

JP 2000511418 T2 20000905 JP 1997-542397 19970516
PRIORITY-APPLN. INFO.: US 1996-651998 A 19960520
WO 1997-US7282 W 19970516

AB Nucleic acids encoding human IL-1.gamma., and purified IL-1.gamma. proteins and fragments thereof are provided. Polyclonal and monoclonal antibodies, both anti-IL-1.gamma. antibodies and anti-idiotypic antibodies which may be agonists or antagonists of human IL-1.gamma., are also provided. Methods of using the compns. for both diagnostic and therapeutic utilities are also provided, together with antagonists and receptors of human IL-1.gamma..

IT 178234-94-1, Interleukin 18 (human)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; structure and antagonists of human interleukin-1.gamma.)

L2 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:689145 HCAPLUS

DOCUMENT NUMBER: 127:357917

TITLE: Involvement of caspase-1 and caspase-3 in the production and processing of mature human interleukin 18 in monocytic THP.1 cells

AUTHOR(S): Akita, Kenji; Ohtsuki, Takashi; Nukada, Yoshiyuki; Tanimoto, Tadao; Namba, Motoshi; Okura, Takanori; Takakura-Yamamoto, Rohko; Torigoe, Kakuji; Gu, Yong; Su, Michael S. -S.; Fujii, Mitsukiyo; Satoh-Itoh, Michiyo; Yamamoto, Kouzo; Kohno, Keizo; Ikeda, Masao; Kurimoto, Masashi

CORPORATE SOURCE: Fujisaki Institute, Hayashibara Biochemical Laboratories, Inc., Okayama, 702, Japan

SOURCE: Journal of Biological Chemistry (1997), 272(42), 26595-26603

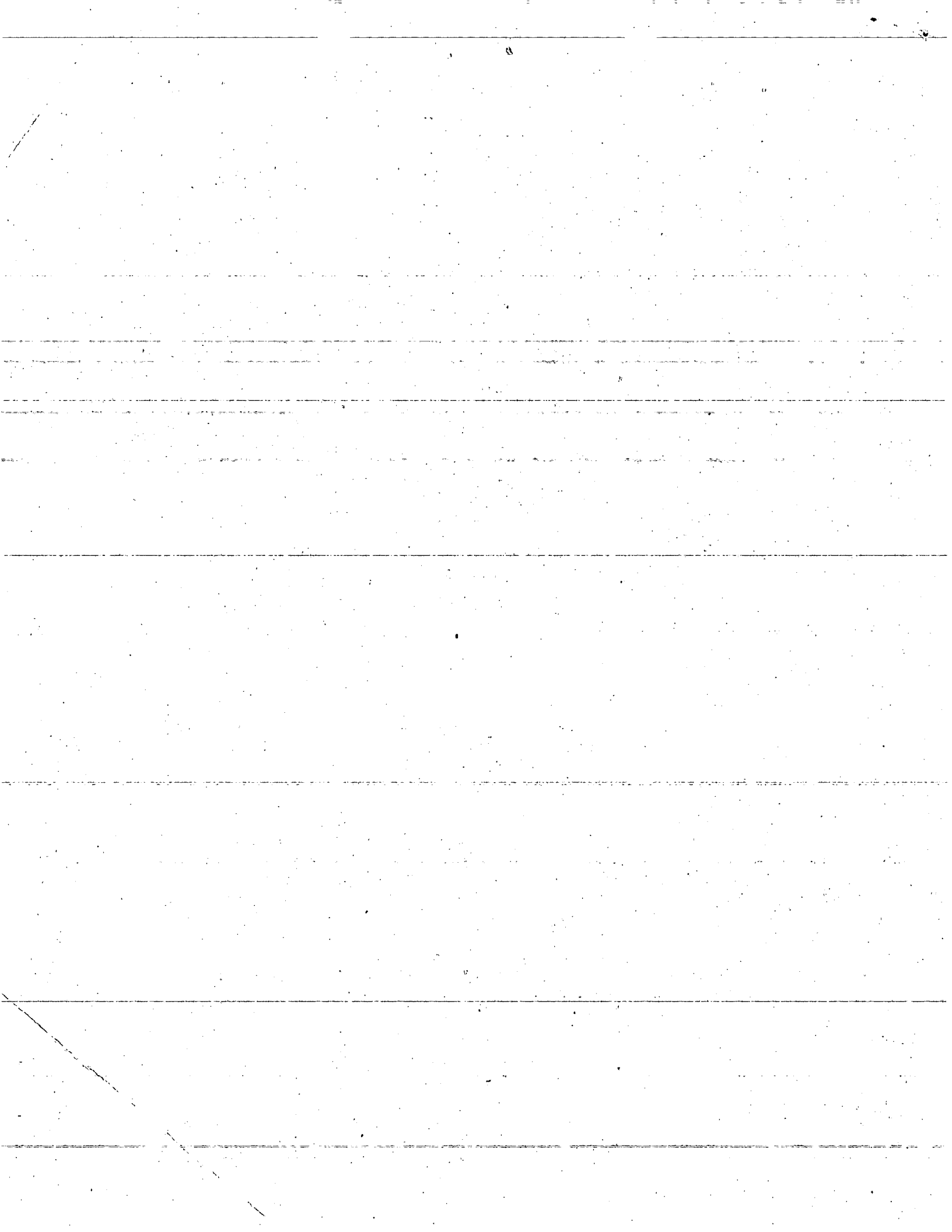
CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recently, human interleukin 18 (hIL-18) cDNA was cloned, and the recombinant protein with a tentatively assigned N-terminal amino acid sequence was generated. However, natural hIL-18 has not yet been isolated, and its cellular processing is therefore still unclear. To clarify this, the authors purified natural hIL-18 from the cytosolic ext. of monocytic THP.1 cells. Natural hIL-18 exhibited a mol. mass of 18.2 kDa, and the N-terminal amino acid was Tyr37. Biol. activities of the purified protein were identical to those of recombinant hIL-18 with respect to the enhancement of natural killer cell cytotoxicity and interferon-.gamma. prodn. by human peripheral blood mononuclear cells. The authors also found two precursor hIL-18 (prohIL-18)-processing activities in the cytosol of THP.1 cells. These activities were blocked sep. by the caspase inhibitors Ac-YVAD-CHO and Ac-DEVD-CHO. Further analyses of the partially purified enzymes revealed that one is caspase-1, which cleaves prohIL-18 at the Asp36-Tyr37 site to generate the mature



09/711896

hIL-18, and the other is caspase-3, which cleaves both precursor and mature hIL-18 at Asp71-Ser72 and Asp76-Asn77 to generate biol. inactive products. Apparently, the prodn. and processing of natural hIL-18 are regulated by two processing enzymes, caspase-1 and caspase-3, in THP.1 cells.

IT 178234-94-1, Interleukin 18 (human)

RL: PRP (Properties)

(caspase-1 and caspase-3 in formation and processing of mature human interleukin 18 in monocytes)

L2 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:526678 HCAPLUS

DOCUMENT NUMBER: 127:148345

TITLE: Human interferon .gamma.-inducing factor-2 cDNA sequence, point mutation, and drug screening and disease diagnosis and therapy

INVENTOR(S): Coleman, Roger; Cocks, Benjamin Graeme; Hawkins, Phillip R.

PATENT ASSIGNEE(S): Incyte Pharmaceuticals, Inc., USA; Coleman, Roger; Cocks, Benjamin Graeme; Hawkins, Phillip R.

SOURCE: PCT Int. Appl., 59 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

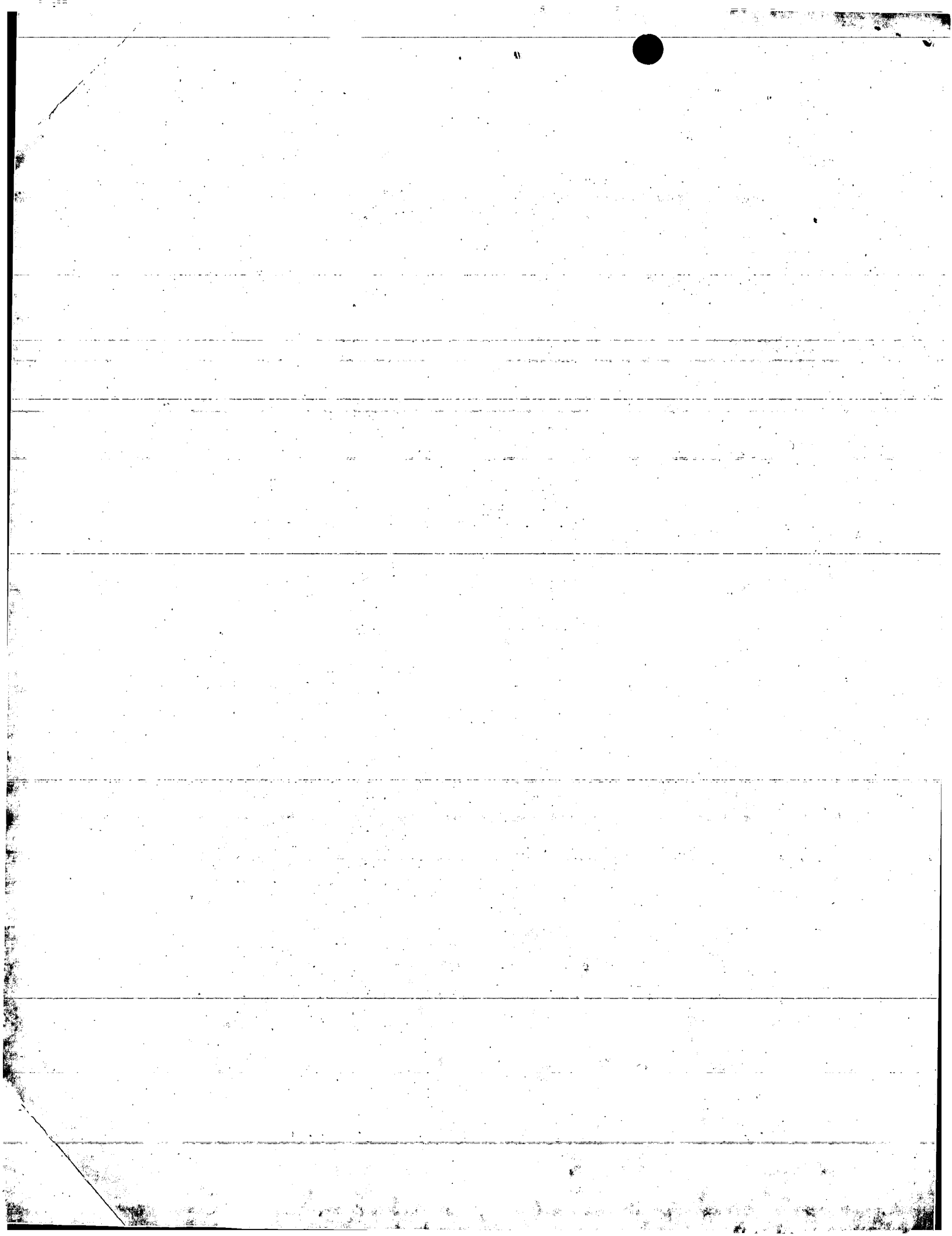
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9724441	A1	19970710	WO 1996-US20432	19961220
W:	AT, AU, BA, BR, CA, CH, CN, DE, DK, ES, FI, GB, IL, JP, KR, LC, MX, NO, NZ, RU, SE, SG, US, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
CA 2238885	AA	19970710	CA 1996-2238885	19961220
AU 9713417	A1	19970728	AU 1997-13417	19961220
EP 870028	A1	19981014	EP 1996-944936	19961220
R:	BE, DE, ES, FR, GB, IT, NL			
JP 2000502903	T2	20000314	JP 1997-524487	19961220
PRIORITY APPLN. INFO.:			US 1995-580667	19951229
			WO 1996-US20432	19961220

AB The present invention provides a polynucleotide (igif-2) which identifies and encodes a novel interferon .gamma.-inducing factor-2 (IGIF-2) which was expressed in adenoid, brain, kidney, liver, lung, skin, synovium, and T-lymphocytes. The present invention also provides for antisense mols. The invention further provides genetically engineered expression vectors and host cells for the prodn. of purified IGIF-2; antibodies, antagonists and inhibitors; and pharmaceutical compns. and methods of treatment based on the polypeptide, its antibodies, antagonists and inhibitors. The invention specifically provides for use of this polypeptide as therapeutic for immunocompromised individuals and as a pos. control in diagnostic assays for the detection of aberrant IGIF-2 expression or altered leukocyte or lymphocyte activity.

IT 178234-94-1P, Interleukin 18 (human) 193294-40-5P



09/711896

193294-41-6P

RL: ANT (Analyte); ARU (Analytical role, unclassified); BOC (Biological occurrence); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; human interferon .gamma.-inducing factor-2 cDNA sequence, point mutation, and drug screening and disease diagnosis and therapy)

L2 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:397243 HCAPLUS

DOCUMENT NUMBER: 125:84660

TITLE: A peptide inducer of interferon .gamma. synthesis and antibodies against and their use in the treatment of interferon .gamma.-susceptible disease

INVENTOR(S): Ushio, Shimpei; Torigoe, Kakuji; Tanimoto, Tadao; Okamura, Haruki; Kunikata, Toshio; Taniguchi, Mutsuko; Kohno, Keizo; Fukuda, Shigeharu; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 48 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 712931	A2	19960522	EP 1995-308055	19951110
EP 712931	A3	19970326		
EP 712931	B1	20010214		
R: BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
JP 08231598	A2	19960910	JP 1995-58240	19950223
JP 2952750	B2	19990927		
JP 08193098	A2	19960730	JP 1995-262062	19950918
JP 2724987	B2	19980309		
JP 10007699	A2	19980113	JP 1997-58547	19950918
TW 464656	B	20011121	TW 1995-84110504	19951004
CA 2162353	AA	19960516	CA 1995-2162353	19951107
EP 962531	A2	19991208	EP 1999-104104	19951110
EP 962531	A3	19991215		
R: BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
ES 2156199	T3	20010616	ES 1995-308055	19951110
AU 9537796	A1	19960523	AU 1995-37796	19951113
AU 700948	B2	19990114		
US 6197297	B1	20010306	US 1995-558818	19951115
JP 09157180	A2	19970617	JP 1996-28722	19960124
US 6214584	B1	20010410	US 1997-832180	19970408
US 6268486	B1	20010731	US 1997-832177	19970408
US 6207641	B1	20010327	US 1997-974469	19971120
US 6509449	B1	20030121	US 2000-711899	20001115
PRIORITY APPLN. INFO.:				
			JP 1994-304203	A 19941115
			JP 1995-58240	A 19950223

Searcher : Shears 308-4994

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JP 1995-78357 A 19950310
JP 1995-262062 A 19950918
JP 1995-274988 A 19950929
JP 1995-279906 A 19951004
EP 1995-308055 A3 19951110
US 1995-558190 B2 19951115
US 1995-558191 A3 19951115
US 1995-558818 A3 19951115
US 1996-599879 B1 19960214

AB A polypeptide of 18,500. \pm 3,000 Da by SDS-PAGE and a pI of 4.9. \pm 1.0 by chromatofocusing that strongly induces the IFN- γ prodn. by immunocompetent cells at low concns. and that does not cause serious side effects even when administered to human in a relatively high dose is described. The protein is readily prepd. by immune affinity chromatog. using a monoclonal antibody and can be incorporated into agents for treating and/or preventing malignant tumors, viral diseases, bacterial infectious diseases, and immune diseases.

IT 178254-43-8P

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(amino acid sequence; peptide inducers of interferon γ synthesis of human and mouse and antibodies against and their use in treatment of interferon γ -susceptible disease)

L2 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:314489 HCAPLUS

DOCUMENT NUMBER: 125:55848

TITLE: Cloning of the cDNA for human IFN- γ -inducing factor, expression in Escherichia coli, and studies on the biologic activities of the protein

AUTHOR(S): Ushio, Shimpei; Namba, Motoshi; Okura, Takanori; Hattori, Kazuko; Nukada, Yoshiyuki; Akita, Kenji; Tanabe, Fujimi; Konishi, Kaori; Micallef, Mark; et al.

CORPORATE SOURCE: Fujisaki Inst., Hayashibara Biochem. Lab., Inc., Okayama, Japan

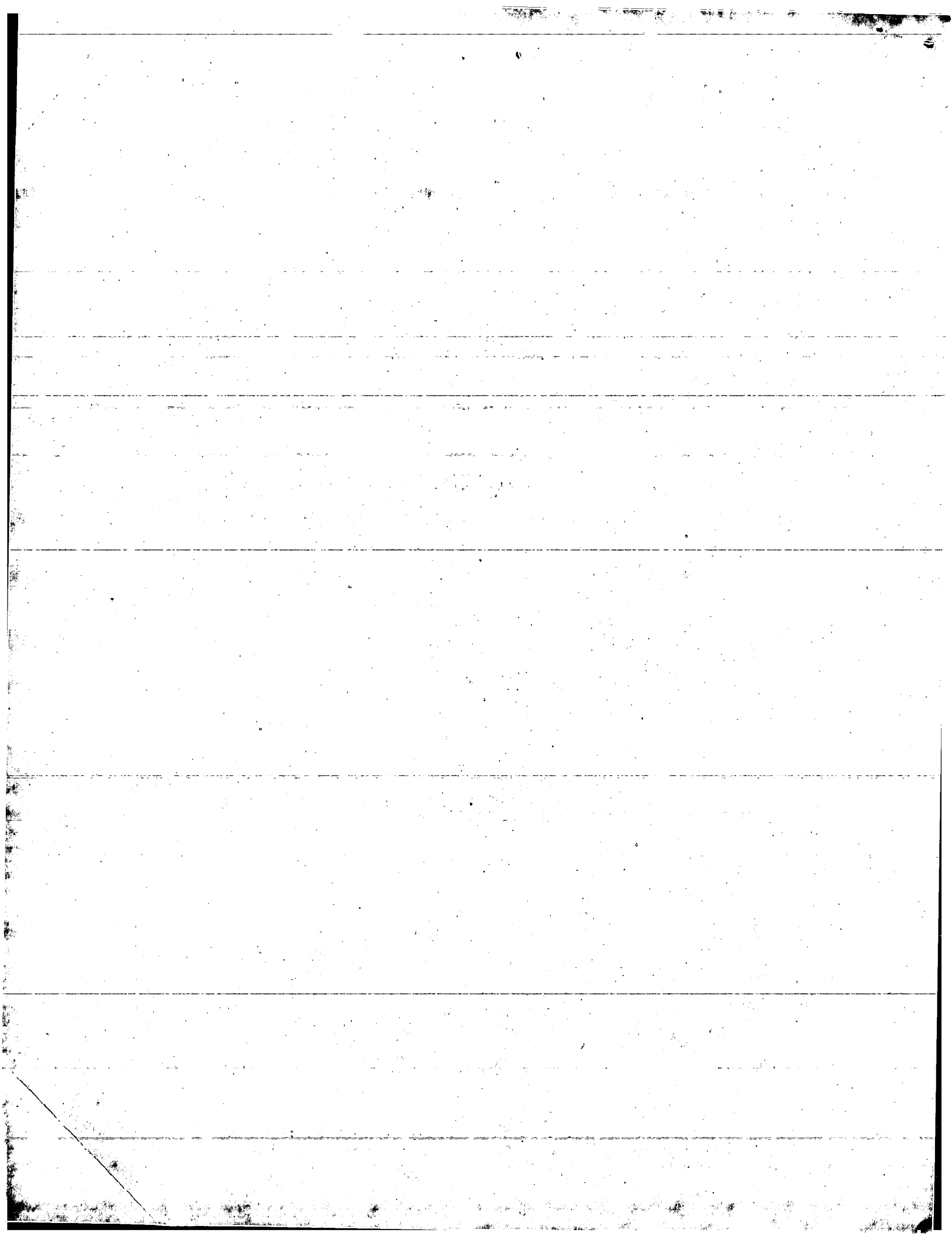
SOURCE: Journal of Immunology (1996), 156(11), 4274-4279
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors have recently reported that a novel mol., murine IFN- γ -inducing factor (IGIF) produced by mouse liver cells, possesses potent biol. activities, including the induction of IFN- γ prodn. by spleen cells and the enhancement of NK cell cytotoxicity. In this paper, the authors report on the isolation of human IGIF cDNA clones from normal human liver cDNA libraries using murine IGIF cDNA as a probe. The amino acid sequence deduced from the human cDNA clones indicated a 193-amino acid precursor peptide and revealed 65% homol. with that of murine IGIF. The amino acid sequence of IGIF also included an IL-1 signature-like sequence. Subsequently, the cloned cDNA was expressed in Escherichia coli, and preliminary studies on the biol. activities of the recombinant



09/711896

protein were performed. The recombinant human IGIF induced IFN-.gamma. prodn. by mitogen-stimulated PBMC and enhanced NK cell cytotoxicity, in a manner similar to murine IGIF. In addn., recombinant human IGIF also augmented granulocyte-macrophage-CSF prodn. and decreased IL-10 prodn., but had no effect on IL-4 prodn. by Con A-stimulated PBMC. Based on these pleiotropic effects of IGIF, the authors propose that this novel cytokine be designated as IL-18.

IT 178234-94-1, Interleukin 18 (human)
RL: PRP (Properties)
(amino acid sequence; cloning of cDNA for human IFN-.gamma.-inducing factor, expression in Escherichia coli, and studies on biol. activities of protein)

E1 THROUGH E11 ASSIGNED

FILE 'REGISTRY' ENTERED AT 10:33:49 ON 23 APR 2003

L3 11 SEA FILE=REGISTRY ABB=ON PLU=ON (178234-94-1/BI OR
178254-43-8/BI OR 202538-32-7/BI OR 202608-43-3/BI OR
193294-40-5/BI OR 193294-41-6/BI OR 263886-60-8/BI OR
341990-01-0/BI OR 383927-79-5/BI OR 480762-83-2/BI OR
480765-89-7/BI)

L4 11 L3 AND L1

L4 ANSWER 1 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 480765-89-7 REGISTRY
CN Interleukin 18 (interferon-gamma-inducing factor) (human clone
MGC:12320 IMAGE:3681009) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAH07461
CN GenBank AAH07461 (Translated from: GenBank BC007461)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDFYFGK LESKLSVIRN
=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIIISFK EMNPPDNIKD TKSDIIFFQR SVPGHDKMKQ
151 FESSSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84318

L4 ANSWER 2 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 480762-83-2 REGISTRY
CN GenBank AAH07007 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAH07007 (Translated from: GenBank BC007007)
CN Interleukin 18 (interferon-gamma-inducing factor) (human clone
MGC:12321 IMAGE:3686124)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDFYFGK LESKLSVIRN

Searcher : Shears 308-4994

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=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84318

L4 ANSWER 3 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 383927-79-5 REGISTRY
CN Interleukin 18 (human precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0198455 SEQID: 1 claimed protein
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
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51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:68716

L4 ANSWER 4 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 341990-01-0 REGISTRY
CN L-Aspartic acid, L-methionyl-L-alanyl-L-alanyl-L-.alpha.-glutamyl-L-prolyl-L-valyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-asparaginyl-L-cysteinyl-L-isoleucyl-L-asparaginyl-L-phenylalanyl-L-valyl-L-alanyl-L-methionyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-.alpha.-aspartyl-L-asparaginyl-L-threonyl-L-leucyl-L-tyrosyl-L-phenylalanyl-L-isoleucyl-L-alanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-asparaginyl-L-leucyl-L-.alpha.-glutamyl-L-seryl-(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: EP1101772 SEQID: 1 claimed protein
CI MAN
SQL 36

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESD
=====

HITS AT: 1-36

REFERENCE 1: 135:4468

L4 ANSWER 5 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 263886-60-8 REGISTRY
CN Interleukin 18 (human clone pQEIL18p precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF077611-derived protein GI 3348071
CI MAN
SQL 193

09/711896

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFDQ GNRPLLEDMT DSDCRDNAPR TIFIIRMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ SED

HITS AT: 1-36

REFERENCE 1: 132:277966

L4 ANSWER 6 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 202608-43-3 REGISTRY
CN Proteinase, interleukin 1.beta. precursor [73-isoleucine] (human
clone pRCHuGF precursor) (9CI) (CA INDEX NAME)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFDQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISIL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

REFERENCE 1: 128:166370

REFERENCE 2: 128:151108

L4 ANSWER 7 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 202538-32-7 REGISTRY
CN L-Leucine, L-methionyl-L-alanyl-L-alanyl-L-.alpha.-glutamyl-L-prolyl-
L-valyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-asparaginyl-L-
cysteinyl-L-isoleucyl-L-asparaginyl-L-phenylalanyl-L-valyl-L-alanyl-
L-methionyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-.alpha.-aspartyl-L-
asparaginyl-L-threonyl-L-leucyl-L-tyrosyl-L-phenylalanyl-L-isoleucyl-
L-alanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-
.alpha.-glutamyl-L-asparaginyl-L-leucyl-L-.alpha.-glutamyl-L-seryl-L-
.alpha.-aspartyl-L-tyrosyl-L-phenylalanylglycyl-L-lysyl- (9CI) (CA
INDEX NAME)
CI MAN
SQL 41

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK L

HITS AT: 1-36

REFERENCE 1: 128:166370

REFERENCE 2: 128:151108

L4 ANSWER 8 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 193294-41-6 REGISTRY
CN Interferon .gamma.-inducing factor-2 (human large isoform) (9CI)
(CA INDEX NAME)
CI MAN
SQL 205

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

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=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NEDGKVMNL
201 FFFAN

HITS AT: 1-36

REFERENCE 1: 127:148345

L4 ANSWER 9 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 193294-40-5 REGISTRY
CN Interferon .gamma.-inducing factor-2 [140-arginine] (human short isoform) (9CI) (CA INDEX NAME)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOI SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

REFERENCE 1: 127:148345

L4 ANSWER 10 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 178254-43-8 REGISTRY
CN Protein (human clone pHIGIF interferon .gamma.-inducing precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: EP1101772 SEQID: 4 claimed protein
CN Interleukin 18 (human precursor)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISXL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

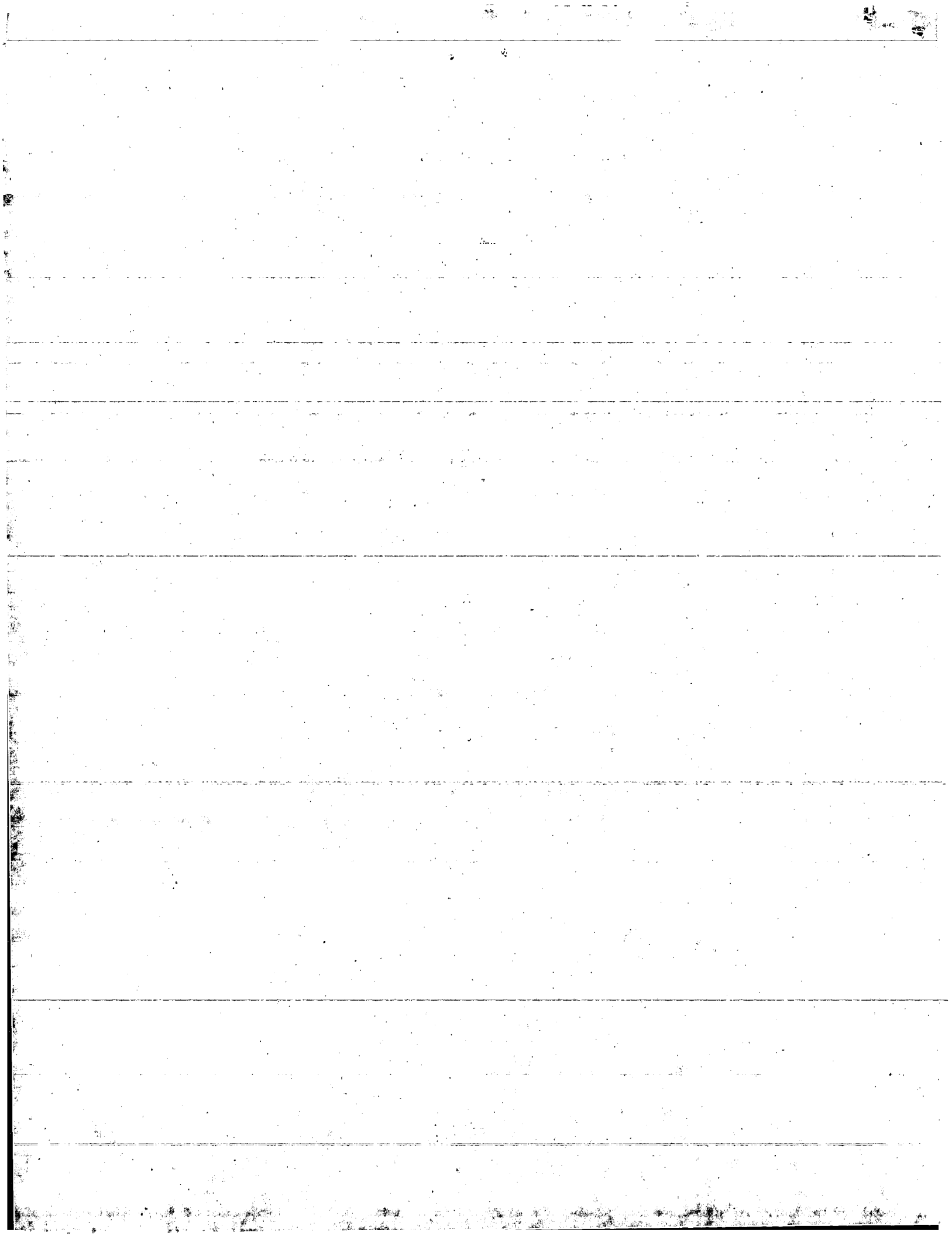
RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:4468

REFERENCE 2: 128:137190

REFERENCE 3: 125:84660

L4 ANSWER 11 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 178234-94-1 REGISTRY
CN Interleukin 18 (human precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0168896 SEQID: 1 unclaimed protein
CN Cytokine IGIF (human precursor)
CN Interferon .gamma.-inducing factor (human precursor)
CN Interferon .gamma.-inducing factor-2 (human short isoform precursor)



09/711896

CN Interleukin 18 (human monocyte precursor)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFIDQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:271914

REFERENCE 2: 128:166370

REFERENCE 3: 128:151108

REFERENCE 4: 128:58316

REFERENCE 5: 127:357917

REFERENCE 6: 127:148345

REFERENCE 7: 125:55848

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